

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:52 ; Search time 147.68 seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20
Sequence: 1 taaggcgttcgataaaccc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents_NA: *
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/lna/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/lna/PCRTS.COMB.seq: *
6: /cgn2_6/ptodata/2/lna/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	432	2	US-08-313-185-59 Sequence 59, Appl
2	20	100.0	432	3	US-09-082-614A-59 Sequence 59, Appl
3	20	100.0	620	2	US-08-757-653-135 Sequence 135, App
4	20	100.0	620	2	US-08-757-653-136 Sequence 136, App
5	20	100.0	620	2	US-08-757-653-137 Sequence 137, App
6	20	100.0	620	2	US-08-757-653-138 Sequence 138, App
7	20	100.0	620	2	US-08-757-653-139 Sequence 139, App
8	20	100.0	620	2	US-08-757-653-140 Sequence 140, App
9	20	100.0	706	4	US-08-797-812-24 Sequence 24, Appl
10	20	100.0	970	1	US-08-250-030-1 Sequence 1, Appl
11	20	100.0	970	5	PCT-US95-06790-1 Sequence 1, Appl
12	19	95.0	19	4	US-08-750-088A-71 Sequence 71, Appl
13	15	75.0	27	5	PCT-US95-06790-9 Sequence 9, Appl
14	15	75.0	27	5	PCT-US95-06790-9 Sequence 9, Appl
15	14	70.0	3447	3	US-09-082-614A-57 Sequence 57, Appl
16	14	70.0	3447	3	US-09-082-614A-57 Sequence 57, Appl
17	13	65.0	383	3	US-08-906-769-169 Sequence 169, App
18	13	65.0	383	3	US-08-906-769-169 Sequence 169, App
19	13	65.0	383	3	US-08-906-769-169 Sequence 169, App
20	13	65.0	383	4	US-09-012-431-169 Sequence 169, App
21	13	65.0	383	4	US-09-012-431-169 Sequence 169, App
22	13	65.0	383	4	US-09-012-692-169 Sequence 169, App
23	13	65.0	537	3	US-08-906-613-169 Sequence 169, App
24	13	65.0	537	3	US-08-906-613-169 Sequence 169, App
25	13	65.0	537	3	US-08-906-616-171 Sequence 171, App
26	13	65.0	537	3	US-08-639-075A-171 Sequence 171, App
27	13	65.0	537	4	US-09-012-431-171 Sequence 171, App

28	13	65.0	537	4	US-08-906-613-171 Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29 Sequence 29, Appl
30	13	65.0	1938	4	US-09-232-197-29 Sequence 29, Appl
31	13	65.0	1938	4	US-09-232-201-29 Sequence 29, Appl
32	13	65.0	3000	2	US-08-896-344A-1 Sequence 1, Appl
33	13	65.0	3000	2	US-09-360-682A-1 Sequence 1, Appl
34	13	65.0	3217	4	US-09-232-200-64 Sequence 64, Appl
35	13	65.0	3217	4	US-09-232-197-64 Sequence 64, Appl
36	13	65.0	3217	4	US-09-232-201-64 Sequence 64, Appl
37	13	65.0	4403765	4	US-09-103-840A-2 Sequence 2, Appl
38	12	60.0	391	1	US-08-636-928-6 Sequence 6, Appl
39	12	60.0	412	4	US-08-976-259-123 Sequence 123, App
40	12	60.0	645	1	US-08-459-586-19 Sequence 19, Appl
41	12	60.0	645	2	US-08-282-696-19 Sequence 19, Appl
42	12	60.0	648	5	PCT-US96-04648-4 Sequence 4, Appl
43	12	60.0	709	1	US-08-459-586-20 Sequence 20, Appl
44	12	60.0	709	2	US-08-282-696-20 Sequence 20, Appl
45	12	60.0	728	4	US-08-998-416-615 Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/C
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bomber, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunne
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/c

Sequence 59, Application US/09082614A

Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Hegm, Beate

APPLICANT: Cole, Stewart

APPLICANT: Young, Douglas

APPLICANT: Zhang, Ying

APPLICANT: Honore, Nadine

APPLICANT: Telenti, Amalio

APPLICANT: Bodmer, Thomas

TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

TITLE OF INVENTION: In Mycobacterium Tuberculosis

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,614A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/313,185

FILING DATE: 12-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356, 0066-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/c

Sequence 135, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medien & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medien & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02365

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:

LENGTH: 620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/c

Sequence 136, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medien & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/C
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
TELEPHONE: (415) 705-8410
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 620;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
US-08-757-653-140
Sequence 140 Application US/08757653
Patent No. 5843869
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
NUMBER OF SEQUENCES: 190
THERMOSTABLE FBN-1 Endonucleases
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
TELEPHONE: (415) 705-8410
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139
```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-140

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 620;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
US-08-797-812-24/C
Sequence 24 Application US/08797812
Patent No. 6228575
GENERAL INFORMATION:
APPLICANT: Gingeras, Thomas A.
APPLICANT: Mack, David
APPLICANT: Chee, Mark S.
APPLICANT: Berne, Anthony J.
APPLICANT: Stryer, Lubert
APPLICANT: Ghandour, Ghassan
TITLE OF INVENTION: Chip-Based Species Identification and
NUMBER OF SEQUENCES: 36
TYPIC Characterization of Microorganisms
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,339
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16528X-018550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 24:
```


This Page Blank (uspto)

130:219116

TI Method of selecting PCR primer pairs to amplify a group of related nucleotide sequences

IN McClelland, Michael; Pesole, Graziano

PA Sidney Kimmel Cancer Center, USA

SO PCT Int. Appl., 92 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9911823	A2	19990311	WO 1998-US18392	19980904
	WO 9911823	A3	19990610		
	W:		AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG		
	AU 9893027	A1	19990322	AU 1998-93027	19980904
	EP 1007739	A2	20000614	EP 1998-945882	19980904
	R:		AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI		
PRAI	US 1997-925816	A	19970905		
	WO 1998-US18392	W	19980904		
AB	The present invention provides a method of detg. a set of primer pairs for amplifying a group of related nucleotide sequences. A method of the invention is performed by identifying a group of related nucleotide sequences; generating the set of primers that matches each of the related nucleotide sequences; detg. for each systematic pairing of each primer which of the related nucleotide sequences are amplified; and selecting from the systematic pairings a subset which amplifies all of the related nucleotide sequences. The invention also provides a method of using a set of primer pairs, which amplify a group of related nucleotide sequences, to identify nucleotide sequences related to the original group of nucleotide sequences. Eight-mer primer pairs are provided for amplification of genes encoding nuclear receptors, G-protein coupled receptors, apoptosis-assocd. proteins, DNA repair enzymes, and replication enzymes. The invention also provides a computer app. for carrying out the computer-executed steps of the method. The invention further provides a computer program product comprising a signal bearing media for carrying out the method.				

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||
Db 332 TAGGCGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c

; Sequence 1, Application US/08250030
; Patent No. 5643723

; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250.030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.

; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||
Db 671 TAGGCGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c

; Sequence 1, Application PC/TUS9506790

; GENERAL INFORMATION:

; APPLICANT: Mayo Foundation for Medical Education and Research

; APPLICANT: and Hoffmann-La Roche Inc.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding

; TITLE OF INVENTION: Resistance to Rifampin

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:
; ADDRESSER: Schwegman, Lundberg & Woessner

; STREET: 3500 IDS Center

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Raasch, Kevin W.

; REGISTRATION NUMBER: 35,651

; REFERENCE/DOCKET NUMBER: 150.105051

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331

; TELEFAX: 612-339-3061

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||

Db 671 TAGGCGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71

; Sequence 71, Application US/08750088A
; Patent No. 6329138

; GENERAL INFORMATION:

; APPLICANT: DE BEENHOUWER, HANS

; APPLICANT: PORTAELS, FRAN OISE

; APPLICANT: MACHTELINCKX, LIEVE

; APPLICANT: JANNES, GEERT

; APPLICANT: ROSSAU, RUDI

; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC

; NUMBER OF SEQUENCES: 71
; RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES

; CORRESPONDENCE ADDRESS:
; ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: US

; ZIP: 20005-3934

; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

;;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tagcggttcgatgaacc 19
DB 1 TACGGCGTTTCGATGAACC 19

RESULT 13
US-08-250-030-9
; Sequence 9, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-030-9

Query Match 75.0%; Score 15; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 cgtttcgatgaacc 20
DB 1 CGTTTCGATGAACC 15

RESULT 14
PCT-US95-06790-9
; Sequence 9, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105WO1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US95-06790-9

Query Match 75.0%; Score 15; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 cgtttcgatgaacc 20
DB 1 CGTTTCGATGAACC 15

RESULT 15
US-08-313-185-57/C
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 70.0%; Score 14; DB 2; Length 3447;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 gttcgatgaacc 20
|||||
Db 1448 GTTCGATGAACCC 1435

Search completed: August 7, 2002, 23:51:54
Job time: 7180 sec



THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:31 ; Search time 562.71 Seconds
(Without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctgcgcgcgcgcgcgc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N_Geneseq_032802.*
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	17	AA112092
2	20	100.0	20	21	AAA49823
3	20	100.0	20	21	AAA49825
4	20	100.0	306	19	AAK27214
5	20	100.0	306	19	AAK27175
6	20	100.0	306	19	AAK27179
7	20	100.0	306	19	AAK27180
8	20	100.0	306	24	AAK27180
9	20	100.0	306	24	AAK27180

10	20	100.0	306	24	AAK27180	Mycobacterium spec
11	20	100.0	306	24	AAK27180	Mycobacterium spec
12	20	100.0	432	14	AAK61457	M. tuberculosis rpo
13	20	100.0	480	21	AAK49863	Mycobacterium tube
14	20	100.0	970	17	AAK09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAH24651	Mycobacterium tube
18	20	100.0	3853	21	AAH24651	Mycobacterium tube
19	19	95.0	306	24	AAK27217	M. tuberculosis rpo
20	19	95.0	306	24	AAK27217	Mycobacterium spec
21	19	95.0	21500	23	AAK59633	Propionibacterium
22	18	90.0	25	17	AAK12091	M. tuberculosis rpo
23	18	90.0	87	22	AAK88922	Mycobacterium tube
24	16	80.0	306	19	AAK27212	RpoB gene fragment
25	16	80.0	306	19	AAK27218	RpoB gene fragment
26	16	80.0	306	19	AAK27193	RpoB gene fragment
27	16	80.0	306	19	AAK27196	RpoB gene fragment
28	16	80.0	306	19	AAK27204	RpoB gene fragment
29	16	80.0	306	19	AAK27177	RpoB gene fragment
30	16	80.0	306	19	AAK27182	RpoB gene fragment
31	16	80.0	306	19	AAK27183	RpoB gene fragment
32	16	80.0	306	19	AAK27186	RpoB gene fragment
33	16	80.0	306	24	AAK59539	Mycobacterium spec
34	16	80.0	306	24	AAK59557	Mycobacterium spec
35	16	80.0	306	24	AAK59560	Mycobacterium spec
36	16	80.0	306	24	AAK59565	Mycobacterium spec
37	16	80.0	306	24	AAK59568	Mycobacterium spec
38	16	80.0	27426	23	AAK59541	Propionibacterium
39	15	75.0	1092	22	AAK502316	B. subtilis DNA en
40	15	75.0	2488	23	ABL14021	Drosophila melanog
41	15	75.0	2772	23	AAK54170	Pseudomonas aerugi
42	15	75.0	4544	23	ABL14020	Drosophila melanog
43	15	75.0	4403765	22	AAK19683	Mycobacterium tube
44	15	75.0	4411529	22	AAK19683	Mycobacterium tube
45	14	70.0	50	19	AAK31045	Expression vector

ALIGNMENTS

RESULT 1	
ID	AA112092
10-JUN-1996	(first entry)
AC	AA112092:
DT	10-JUN-1996 (first entry)
DE	M. tuberculosis rpoB gene fragment amplification primer P2.
XX	
KW	Antibiotic; resistance; spectrum; gene; mycobacterium;
KW	determination; amplification; tuberculosis; rpoB; fragment;
KW	primer; differential; hybridisation; pattern; rifampicin;
KW	rifabutin; species identification; ss.
OS	Synthetic.
XX	
PN	MO539851-A2
PN	14-DEC-1995.
PD	
XX	
PE	09-JUN-1995; 95WO-EP02230.
XX	
PR	09-JUN-1994; 94EP-0870093.
XX	
PA	(INNO-) INNOGENETICS NV.
XX	
PI	De Beenhouwer H, Jannes G, Machtelincx L, Portaeals F;
PI	Rosau R;
XX	
DR	WPI; 1996-040250/04.
XX	

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
XX different patterns of hybridisation with rpoB gene
PS Claim 22; Page 39; 69pp; English.

XX The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.

SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcgagctgacc 20
DB 1 tacggtcgagcgagctgacc 20

RESULT 2
AAA49823 standard; DNA; 20 BP.

AC AAA49823;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 4; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the presence of M.
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcgagctgacc 20
DB 1 tacggtcgagcgagctgacc 20

RESULT 3
AAA49825 standard; DNA; 20 BP.

AC AAA49825;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 5; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826
CC and with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the presence of *katG*, *isrA*, *isrB*
CC and *23S* genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match	100.0%	Score 20:	DB 21:	Length 20:
Best Local Similarity	100.0%	Pred. No.	0.031:	
Matches	20:	Mismatches	0:	Indels 0:
				Gaps 0:

Qy	1	tacggtcgcgagctgattcc	20
Db	1	tacggtcgcgagctgattcc	20

```

RESULT      4
AAx27214
ID   AAx27214 standard; DNA; 306 BP.

```

AC	AAx27214;
XX	
DT	27-MAY-1999 (first entry)

KM RpoB gene; mycobacteria; phylogenetic tree construction;
KW mycobacterial species identification; phylogenetic analysis; ss.

OS Mycobacteria tuberculosis.

PN W09905316-A1

PD 04-FEB-1999.

PF 28-JUL-1998; 98KR-0000228.

PR 28-JUL-1997; 97KR-0035501.

PA (BION-) BIONEER CORP.

PI K1m B, Kook Y;

DR WPI; 1998-539367/46.

PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *ipob* gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
X5
X6
X7
X8
X9
X10
X11
X12
X13
X14
X15
X16
X17
X18
X19
X20
X21
X22
X23
X24
X25
X26
X27
X28
X29
X30
X31
X32
X33
X34
X35
X36
X37
X38
X39
X40
X41
X42
X43
X44
X45
X46
X47
X48
X49
X50
X51
X52
X53
X54
X55
X56
X57
X58
X59
X60
X61
X62
X63
X64
X65
X66
X67
X68
X69
X70
X71
X72
X73
X74
X75
X76
X77
X78
X79
X80
X81
X82
X83
X84
X85
X86
X87
X88
X89
X90
X91
X92
X93
X94
X95
X96
X97
X98
X99
X100
X101
X102
X103
X104
X105
X106
X107
X108
X109
X110
X111
X112
X113
X114
X115
X116
X117
X118
X119
X120
X121
X122
X123
X124
X125
X126
X127
X128
X129
X130
X131
X132
X133
X134
X135
X136
X137
X138
X139
X140
X141
X142
X143
X144
X145
X146
X147
X148
X149
X150
X151
X152
X153
X154
X155
X156
X157
X158
X159
X160
X161
X162
X163
X164
X165
X166
X167
X168
X169
X170
X171
X172
X173
X174
X175
X176
X177
X178
X179
X180
X181
X182
X183
X184
X185
X186
X187
X188
X189
X190
X191
X192
X193
X194
X195
X196
X197
X198
X199
X200
X201
X202
X203
X204
X205
X206
X207
X208
X209
X210
X211
X212
X213
X214
X215
X216
X217
X218
X219
X220
X221
X222
X223
X224
X225
X226
X227
X228
X229
X230
X231
X232
X233
X234
X235
X236
X237
X238
X239
X240
X241
X242
X243
X244
X245
X246
X247
X248
X249
X250
X251
X252
X253
X254
X255
X256
X257
X258
X259
X260
X261
X262
X263
X264
X265
X266
X267
X268
X269
X270
X271
X272
X273
X274
X275
X276
X277
X278
X279
X280
X281
X282
X283
X284
X285
X286
X287
X288
X289
X290
X291
X292
X293
X294
X295
X296
X297
X298
X299
X300
X301
X302
X303
X304
X305
X306
X307
X308
X309
X310
X311
X312
X313
X314
X315
X316
X317
X318
X319
X320
X321
X322
X323
X324
X325
X326
X327
X328
X329
X330
X331
X332
X333
X334
X335
X336
X337
X338
X339
X340
X341
X342
X343
X344
X345
X346
X347
X348
X349
X350
X351
X352
X353
X354
X355
X356
X357
X358
X359
X360
X361
X362
X363
X364
X365
X366
X367
X368
X369
X370
X371
X372
X373
X374
X375
X376
X377
X378
X379
X380
X381
X382
X383
X384
X385
X386
X387
X388
X389
X390
X391
X392
X393
X394
X395
X396
X397
X398
X399
X400
X401
X402
X403
X404
X405
X406
X407
X408
X409
X410
X411
X412
X413
X414
X415
X416
X417
X418
X419
X420
X421
X422
X423
X424
X425
X426
X427
X428
X429
X430
X431
X432
X433
X434
X435
X436
X437
X438
X439
X440
X441
X442
X443
X444
X445
X446
X447
X448
X449
X450
X451
X452
X453
X454
X455
X456
X457
X458
X459
X460
X461
X462
X463
X464
X465
X466
X467
X468
X469
X470
X471
X472
X473
X474
X475
X476
X477
X478
X479
X480
X481
X482
X483
X484
X485
X486
X487
X488
X489
X490
X491
X492
X493
X494
X495
X496
X497
X498
X499
X500
X501
X502
X503
X504
X505
X506
X507
X508
X509
X510
X511
X512
X513
X514
X515
X516
X517
X518
X519
X520
X521
X522
X523
X524
X525
X526
X527
X528
X529
X530
X531
X532
X533
X534
X535
X536
X537
X538
X539
X540
X541
X542
X543
X544
X545
X546
X547
X548
X549
X550
X551
X552
X553
X554
X555
X556
X557
X558
X559
X560
X561
X562
X563
X564
X565
X566
X567
X568
X569
X570
X571
X572
X573
X574
X575
X576
X577
X578
X579
X580
X581
X582
X583
X584
X585
X586
X587
X588
X589
X590
X591
X592
X593
X594
X595
X596
X597
X598
X599
X600
X601
X602
X603
X604
X605
X606
X607
X608
X609
X610
X611
X612
X613
X614
X615
X616
X617
X618
X619
X620
X621
X622
X623
X624
X625
X626
X627
X628
X629
X630
X631
X632
X633
X634
X635
X636
X637
X638
X639
X640
X641
X642
X643
X644
X645
X646
X647
X648
X649
X650
X651
X652
X653
X654
X655
X656
X657
X658
X659
X660
X661
X662
X663
X664
X665
X666
X667
X668
X669
X670
X671
X672
X673
X674
X675
X676
X677
X678
X679
X680
X681
X682
X683
X684
X685
X686
X687
X688
X689
X690
X691
X692
X693
X694
X

This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16S rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in *M. tuberculosis*.

SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match	100.0%	Score 20:	DB 19;	Length 306;
Best Local Similarity	100.0%	Pred. NO.	0.025;	
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
Qy 1 tacgctcgcgagctgattcc 20
    |||
Db 5 tacgctcgcgagctgattcc 24
```

RESULT	5
AAx27175	
ID	AAx27175 standard; DNA; 306 BP

AC	AAx27175;
XX	
DT	27-MAY-1999 (first entry)

KM RpoB gene; mycobacteria; phylogenetic tree construction;
 KM mycobacterial species identification; phylogenetic analysis; ss

OS *Mycobacteria africanum*.

PN WO9905316-A1.

PD 04-FEB-1999.

PF 28-JUL-1998; 98KR-0000228.

PR 28-JUL-1997; 97KR-0035501.

PA (BION-) BIONEER CORP.

PI Kim B, Kook Y;

DR WPI; 1998-539367/46.

PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *iroB* gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
XX
XX Claim 4; Page 62-63; 91pp; English.
XX

CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
CC

SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match	100.0%	Score 20;	DB 19;	Length 306;
Best Local Similarly	100.0%;	Pred. No. 0.025;		
Matches 20; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	tacgctcgcgagctgattcc	20
Db	5	tacgctcgcgagctgattcc	24

AA27179

```

ID  AAX27179 standard; DNA; 306 BP.
XX
XX  AAX27179;
AC
XX  27-MAY-1999 (first entry)
DT
XX
XX  RPOB gene fragment.
DE
XX
XX  RPOB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
XX  Mycobacteria bovis.
OS
XX
XX  WO905316-A1.
PN
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
XX
XX  Claim 8; Page 64; 91pp; English.
PS
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterising these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ

```

Query Match 100.0%; Score 20; DB 19; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY  1 tacgctcggcagctgatcc 20
    |||
DB  5 tacgctcggcagctgatcc 24

```

RESULT 7
 AAX27180
 ID AAX27180 standard; DNA; 306 BP.
 XX
 AC AAX27180;
 XX
 DT 27-MAY-1999 (first entry)
 XX
 XX RPOB gene fragment.
 DE
 XX RPOB gene; mycobacteria; phylogenetic tree construction;
 KM mycobacterial species identification; phylogenetic analysis; ss.
 XX
 OS Mycobacteria bovis.
 XX

```

PN  WO905316-A1.
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
XX
XX  Claim 9; Page 64; 91pp; English.
PS
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterising these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

```

Query Match 100.0%; Score 20; DB 19; Length 306;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY  1 tacgctcggcagctgatcc 20
    |||
DB  5 tacgctcggcagctgatcc 24

```

RESULT 8
 AAS99526
 ID AAS99526 standard; DNA; 306 BP.
 XX
 AC AAS99526;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 XX Mycobacterium species identification primer #1.
 DE
 XX Drug resistance detection: mycobacterial species identification; probe;
 KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
 KW primer.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200192573-A1.
 XX
 PD 06-DEC-2001.
 PD
 XX 30-MAY-2001; 2001WO-KR00904.
 PF
 XX 30-MAY-2000; 2000KR-0029369.
 PR
 XX (BION-) BIOMEDLAB CO LTD.
 PA
 XX Kim H, Kim N, Yoon S, Kim J, Park M;
 PI
 XX

DR WPI: 2002-075472/10.
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
PS Disclosure: Page 21; 74pp; English.
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgacc 20
|||||
DB 5 tacggtcgcgcagctgacc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
XX 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
XX Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.
XX
OS Mycobacterium africanum.
XX
XX WO200192573-A1.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-KR00904.
XX
XX 30-MAY-2000; 2000KR-0029369.
XX
XX (BIOM-) BIOMEDLAB CO LTD.
XX
XX Kim H, Kim N, Yoon S, Kim J, Park M;
XX
XX WPI: 2002-075472/10.
XX
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
XX Disclosure: Page 21; 74pp; English.

XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgacc 20
|||||
DB 5 tacggtcgcgcagctgacc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
XX 12-MAR-2002 (first entry)
XX
XX Mycobacterium species identification primer #5.
XX
DE Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.
XX
OS Mycobacterium bovis.
XX
XX WO200192573-A1.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-KR00904.
XX
XX 30-MAY-2000; 2000KR-0029369.
XX
XX (BIOM-) BIOMEDLAB CO LTD.
XX
XX Kim H, Kim N, Yoon S, Kim J, Park M;
XX
XX WPI: 2002-075472/10.
XX
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
XX Disclosure: Page 21; 74pp; English.
XX
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcgagctgattcc 20
|||||
Db 5 tacgctcgagcgagctgattcc 24

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX

DT 12-MAR-2002 (first entry)
XX

DE Mycobacterium species identification primer #6.
XX

KW Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.

OS Mycobacterium bovis.
XX

PN WO200192573-A1.
XX

PD 06-DEC-2001.
XX

PF 30-MAY-2001; 2001WO-KR00904.
XX

PR 30-MAY-2000; 2000KR-0029369.
XX

PA (BIOM-) BIOMEDLAB CO LTD.
XX

PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX

DR WPI; 2002-075472/10.
XX

PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX

PS Disclosure; Page 21; 74pp; English.
XX

XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcgagctgattcc 20
|||||
Db 5 tacgctcgagcgagctgattcc 24

RESULT 12
AA061457
ID AA061457 standard; DNA; 432 BP.
XX
AC AA061457;
XX

DT 17-MAY-1994 (first entry)
XX

DE M. tuberculosis rpoB gene fragment.
XX

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX

OS Mycobacterium tuberculosis.
XX

PN WO9322454-A.
XX

PD 11-NOV-1993.
XX

PF 30-APR-1993; 93WO-EP01063.
XX

PR 17-SEP-1992; 92FR-0011098.
XX

PR 30-APR-1992; 92US-0875940.
XX

PR 14-AUG-1992; 92US-0929206.
XX

PR 16-APR-1993; 93FR-0004545.
XX

PA (ASSI-) ASSISTANCE PUBLIQUE.
XX

PA (INST PASTEUR.
XX

PA (MEDIT-) MEDICAL RES COUNCIL.
XX

PA (UYBE-) UNIV BERNE.
XX

PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX

PI Young D, Zhang Y;
XX

DR WPI; 1993-368812/46.
XX

DR P-PSDB; AARS1372.
XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX

PS Example 2; Fig 13; 97pp; English.
XX

XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC mutation was isolated from M. tuberculosis (AA061457). A common
CC substitution, most frequently by Leu.
XX

SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcgagctgattcc 20

```
Db 18 tacggtcgcgcgcgtcatcc 37
|||||
RESULT 13
AAA49863
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FH primer_bind complement(41..60)
FT /tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
FT Method for the detection and characterization of Mycobacterium
FT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure: Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-ephc PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y 1 tacggtcgcgcgcgtcatcc 20
```

```
Db 41 tacggtcgcgcgcgtcatcc 60
|||||
RESULT 14
AAT09676
ID AAT09676 standard; DNA; 970 BP.
XX
AC AAT09676;
XX
DT 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
XX polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FH primer_bind 10..27
FT /tag= a
FT /note= "primer FENLRF"
FT primer_bind 226..243
FT /tag= b
FT /note= "primer DDIDHL"
FT primer_bind 226..240
FT /tag= c
FT /note= "primer DDIDH"
FT primer_bind 338..364
FT /tag= d
FT /note= "primer rpo95"
FT primer_bind 348..373
FT /tag= e
FT /note= "primer rpo105"
FT primer_bind 354..373
FT /tag= f
FT /note= "primer KY290"
FT misc_feature 372..373
FT /tag= g
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 433..434
FT /tag= h
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 438
FT /tag= i
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 468..469
FT /tag= j
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 486
FT /tag= k
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 501
FT /tag= l
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 516
FT /tag= m
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 516..535
FT /tag= n
FT /note= "primer rpo273"
FT misc_feature 525
FT /tag= o
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 525..541
FT /tag= p
FT /note= "primer KY292"
FT primer_bind 536..562
FT /tag= q
FT /note= "primer rpo293"
FT primer_bind 640..666
FT /tag= r
```

```

FT primer_bind /note="primer rpo397"
FT primer_bind 952..966
FT primer_bind /*tag= s
FT primer_bind /note="primer NMORO-1"
FT primer_bind 952..966
FT primer_bind /*tag= t
FT primer_bind /note="primer NMORO-2"
PN MO9533074-A1.
XX 07-DEC-1995.
XX
XX
XX 26-MAY-1995; 95MO-US06790.
XX
XX 26-MAY-1994; 94US-0250030.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX Young KRY;
XX WPI; 1996-030581/03.
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Disclosure; Fig.3; 54pp; English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The 1st several bases comprise a
XX nonhybridizing tail consisting of filler bases followed by
XX a restriction site incorporated to facilitate cloning using the
XX amplicon at a later date, if desired. The remaining bases hybridize
XX to bacterial rpoB DNA. The method provides for the detection of M.
XX tuberculosis and the concurrent determination of its drug
XX susceptibility, particularly to rifampin. The method can provide
XX often greater than 95% sensitivity and 100% specificity. The
XX biological sample is a fluid or tissue sample from a human.
XX
XX Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 17; Length 970;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcgagcagctgattcc 20
XX |||||||||||||||||||
XX Db 261 tacggtcgagcagctgattcc 280
XX
XX
XX RESULT 15
XX AAH51976
XX ID AAH51976 standard; DNA; 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX OS
XX XX
XX PN MO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000MO-US31152.
XX
XX

```

```

PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI; 2001-329193/34.
XX
XX P-PSDB; AAG81125.
XX
XX
XX PT Identifying nucleotide or polypeptide sequence for use as drug target,
XX PT involves providing algorithm that analyzes a functional relationship
XX PT between nucleotide or polypeptide sequences, and comparing the
XX PT sequences
XX
XX PS Disclosure; Page 68-69; 207pp; English.
XX
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX algorithm capable of analysing a functional relationship between
XX nucleotide and polypeptide sequences. The method is useful for
XX characterising the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3519;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcgagcagctgattcc 20
XX |||||||||||||||||||
XX Db 1119 tacggtcgagcagctgattcc 1138
XX
XX

```

Search completed: August 8, 2002, 00:01:21
 Job time: 7610 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:45 ; Search time 147.68 Seconds

(Without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20
Sequence: 1 tacggcgttcgatgaacc 20

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents.NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	432	2	US-08-313-185-59
C 2	20	100.0	432	3	US-09-082-614A-59
C 3	20	100.0	620	2	US-08-757-653-135
C 4	20	100.0	620	2	US-08-757-653-136
C 5	20	100.0	620	2	US-08-757-653-137
C 6	20	100.0	620	2	US-08-757-653-138
C 7	20	100.0	620	2	US-08-757-653-139
C 8	20	100.0	620	2	US-08-757-653-140
C 9	20	100.0	706	4	US-08-797-812-24
C 10	20	100.0	970	1	US-08-250-030-1
C 11	20	100.0	970	5	PCT-US95-06790-1
C 12	19	95.0	19	4	US-08-750-088A-71
C 13	15	75.0	27	1	US-08-250-030-9
C 14	15	75.0	27	5	PCT-US95-06790-9
C 15	14	70.0	3447	2	US-08-313-185-57
C 16	14	70.0	3447	3	US-09-082-614A-57
C 17	13	65.0	383	3	US-08-906-616-169
C 18	13	65.0	383	3	US-08-906-616-169
C 19	13	65.0	383	3	US-08-906-616-169
C 20	13	65.0	383	4	US-09-012-431-169
C 21	13	65.0	383	4	US-09-012-431-169
C 22	13	65.0	383	4	US-09-012-692-169
C 23	13	65.0	337	3	US-08-906-613-169
C 24	13	65.0	337	3	US-08-906-616-171
C 25	13	65.0	537	3	US-08-906-616-171
C 26	13	65.0	537	4	US-09-012-431-171
C 27	13	65.0	537	4	US-09-012-692-171

28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, App1
30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, App1
31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, App1
C 32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, App1
C 33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, App1
C 34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, App1
C 35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, App1
C 36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, App1
C 37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, App1
C 38	13	60.0	391	1	US-08-636-928-6	Sequence 123, App
C 39	12	60.0	412	4	US-08-976-259-123	Sequence 19, App1
C 40	12	60.0	645	1	US-08-459-586-19	Sequence 19, App1
C 41	12	60.0	645	2	US-08-282-686-19	Sequence 4, App1
C 42	12	60.0	648	5	PCT-US96-04648-4	Sequence 20, App1
C 43	12	60.0	709	1	US-08-459-586-20	Sequence 20, App1
C 44	12	60.0	709	2	US-08-282-696-20	Sequence 615, App
C 45	12	60.0	728	4	US-08-998-416-615	

ALIGNMENTS

RESULT 1
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Teleni, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313, 185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 428 TACGCGCTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/C
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 428 TACGCGCTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/C
; Sequence 135, Application US/08757653
; Patent No. 5843669

GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGCGCTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/C
; Sequence 136, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/C
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States Of America
;; ZIP: 94104
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,653
;;
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 139:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-139

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgacc 20
|||||
Db 325 TACGGCGTTTCATGACCC 344

RESULT 8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-140

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgacc 20
|||||
Db 325 TACGGCGTTTCATGACCC 344

RESULT 9
US-08-797-812-24/C
; Sequence 24, Application US/08797812
; Patent No. 6228575
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas A.
; APPLICANT: Mack, David
; APPLICANT: Chee, Mark S.
; APPLICANT: Berno, Anthony J.
; APPLICANT: Stryer, Lubert
; APPLICANT: Ghandour, Chassan
; APPLICANT: Wang, Ching
; TITLE OF INVENTION: Chip-Based Species Identification and
; TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,812
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,765
; FILING DATE: 15-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/629,031
; FILING DATE: 08-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,631
; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,339
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Filts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16528X-018550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723

GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-la Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.10501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138

GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657,0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgattgaacc 19
Db 1 TACGGCGCTTCGATTGAACC 19

RESULT 13
US-08-250-030-9
Sequence 9, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150,105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-9

Query Match 75.0%; Score 15; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 14
PCT-US95-06790-9
Sequence 9, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150,105W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-9

Query Match 75.0%; Score 15; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 15
US-08-313-185-57/C
Sequence 57, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

;; TITLE OF INVENTION: In Mycobacterium Tuberculosis
;; NUMBER OF SEQUENCES: 66
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/313,185
;; FILING DATE: 12-OCT-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 02356.0068-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3447 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;;
US-08-313-185-57

Query Match 70.0%; Score 14; DB 2; Length 3447;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gttcgaatgaacc 20
|||||
Db 1448 GTTCGATGAMACC 1435

Search completed: August 7, 2002, 23:51:48
Job time: 7174 sec

THIS PAGE IS BLANK

[illegible]

PT Probes and primers for determin. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrid formed and
CC interfering the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgagcgagctgacc 20
Db 1 tacggtcgagcgagctgacc 20
XX
RESULT 2
AAAA9823
ID AAA49823 standard; DNA: 20 BP.
XX
AC AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KM ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgagcgagctgacc 20
Db 1 tacggtcgagcgagctgacc 20
XX
RESULT 3
AAAA9825
ID AAA49825 standard; DNA: 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-58.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-58 (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpob*, *katG*, *rrsL*/512
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggtcgcgcagctgaccc 20
Db 1 tacggtcgcgcagctgaccc 20
|||||

RESULT 4
ID AAX27214 standard; DNA: 306 BP.
XX
AC AAX27214;
XX
DT 27-MAY-1999 (first entry)
XX
DE *rpob* gene fragment.
XX
KW *rpob* gene: *mycobacteria*; phylogenetic tree construction;
KM *mycobacterial* species identification; phylogenetic analysis; ss.
XX
OS *Mycobacteria tuberculosis*.
XX
PN W09905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpob* gene from *mycobacterial*
PT species, useful for detecting and identifying *mycobacterial* species
XX
PS Claim 43; Page 75-76; 91pp; English.
XX
SQ This sequence represents a *mycobacterial* *rpob* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying *mycobacterial* species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpob* gene (encoding the beta
CC subunit of RNA polymerase) from *mycobacterial* species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the *rpob* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable *mycobacteria*. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggtcgcgcagctgaccc 20
Db 5 tacggtcgcgcagctgaccc 24
|||||

RESULT 5
ID AAX27175 standard; DNA: 306 BP.
XX
AC AAX27175;
XX
DT 27-MAY-1999 (first entry)
XX
DE *rpob* gene fragment.
XX
KW *rpob* gene: *mycobacteria*; phylogenetic tree construction;
KM *mycobacterial* species identification; phylogenetic analysis; ss.
XX
OS *Mycobacteria africanum*.
XX
PN W09905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpob* gene from *mycobacterial*
PT species, useful for detecting and identifying *mycobacterial* species
XX
PS Claim 4; Page 62-63; 91pp; English.
XX
SQ This sequence represents a *mycobacterial* *rpob* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying *mycobacterial* species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpob* gene (encoding the beta
CC subunit of RNA polymerase) from *mycobacterial* species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the *rpob* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable *mycobacteria*. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggtcgcgcagctgaccc 20
Db 5 tacggtcgcgcagctgaccc 24
|||||

RESULT 6
ID AAX27179

```

ID  AAX27179 standard; DNA; 306 BP.
XX
AC  AAX27179;
XX
DT  27-MAY-1999 (first entry)
XX
DE  RpoB gene fragment.
XX
KM  RpoB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
OS  Mycobacteria bovis.
XX
PN  WO905316-A1.
XX
PD  04-FEB-1999.
XX
PF  28-JUL-1998; 98KR-0000228.
XX
PR  28-JUL-1997; 97KR-0035501.
XX
PA  (BION-) BIONEER CORP.
XX
PI  Kim B, Kook Y;
XX
DR  WPI; 1998-539367/46.
XX
PT  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
PS  Claim 8; Page 64; 91pp; English.
XX
CC  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ  Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 tacggtcgcgcgagctgacc 20
    |||
Db  5 tacggtcgcgcgagctgacc 24

RESULT 7
AAX27180
ID  AAX27180 standard; DNA; 306 BP.
XX
AC  AAX27180;
XX
DT  27-MAY-1999 (first entry)
XX
DE  RpoB gene fragment.
XX
KM  RpoB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
OS  Mycobacteria bovis.
XX

```

```

PN  WO905316-A1.
XX
PD  04-FEB-1999.
XX
PF  28-JUL-1998; 98KR-0000228.
XX
PR  28-JUL-1997; 97KR-0035501.
XX
PA  (BION-) BIONEER CORP.
XX
PI  Kim B, Kook Y;
XX
DR  WPI; 1998-539367/46.
XX
PT  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
PS  Claim 9; Page 64; 91pp; English.
XX
CC  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
SQ  Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 tacggtcgcgcgagctgacc 20
    |||
Db  5 tacggtcgcgcgagctgacc 24

RESULT 8
AAS99526
ID  AAS99526 standard; DNA; 306 BP.
XX
AC  AAS99526;
XX
DT  12-MAR-2002 (first entry)
XX
DE  Mycobacterium species identification primer #1.
XX
KM  Drug resistance detection; mycobacterial species identification; probe;
KM  oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KM  primer.
XX
OS  Mycobacterium tuberculosis.
XX
PN  WO200192573-A1.
XX
PD  06-DEC-2001.
XX
PF  30-MAY-2001; 2001WO-KR00904.
XX
PR  30-MAY-2000; 2000KR-0029369.
XX
PA  (BION-) BIOMEDLAB CO LTD.
XX
PI  Kim H, Kim N, Yoon S, Kim J, Park M;
XX

```

DR	WPI; 2002-075472/10.
PX	
PT	Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probe, a mycobacterial drug-resistance detection probe, and its contrast group probe -
PT	
PX	
PS	Disclosure; Page 21; 74pp; English.
XX	
CC	The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium species identification probes and primers of the invention.
CC	
CC	
CC	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ	
PX	
Query Match	100.0%; Score 20; DB 24; Length 306;
Best Local Similarity	100.0%; Pred. NO. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 tacggtcgcgcagctcatcc 20
DB	5 tacggtcgcgcagctcatcc 24
RESULT 9	
AAS99527	
ID AAS99527	standard; DNA: 306 BP.
XX	
AC AAS99527;	
XX	
DT 12-MAR-2002	(first entry)
XX	
DE Mycobacterium species identification primer #2.	
XX	
KW Drug resistance detection; mycobacterial species identification; probe; oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss; primer.	
KM	
KH	
OS Mycobacterium africanum.	
XX	
PN MO2001.92573-A1.	
PD	
PD 06-DEC-2001.	
XX	
PF 30-MAY-2001; 2001WO-KR00904.	
XX	
PR 30-MAY-2000; 2000KR-0029369.	
XX	
PA (BIOM-) BIOMEDLAB CO LTD.	
PX	
PL Kim H, Kim N, Yoon S, Kim J, Park M;	
XX	
DR WPI; 2002-075472/10.	
XX	
PT Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probe, a mycobacterial drug-resistance detection probe, and its contrast group probe -	
PT	
PX	
PS Disclosure; Page 21; 74pp; English.	

CC	The invention relates to a diagnostic kit for mycobacterial species						
CC	identification and drug resistance detection comprising an						
CC	oligonucleotide chip including a species identification probe, a						
CC	mycobacterial drug-resistance detection probe, a contrast group probe						
CC	corresponding to each drug resistance detection probe, and a marker for						
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The						
CC	identification probe is comprised of species-specific DNA sequences of						
CC	mycobacterial rpoB gene and the detection probe is comprised of one or						
CC	more modified codons of mycobacterial rpoB gene. The method involves						
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction						
CC	(PCR) and discriminating species by fluorescent intensity corresponding						
CC	to a particular species. The specimen is preferably uncultured sputum,						
CC	blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569						
CC	represent mycobacterium species identification probes and primers of the						
CC	invention.						
XX							
SQ	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;						
<hr/>							
Query Match	100.0%; Score 20; DB 24; Length 306;						
Best Local Similarity	100.0%; Pred. No. 1,6; Mismatches	0;	Indels	0			
Matches	20; Conservative	0;	Gaps	0			
Oy	1 tacggtcggcgagctgatcc 20 						
Db	5 tacggtcggcgagctgatcc 24						
<hr/>							
RESULT 10							
AAS99530							
ID	AAS99530 standard; DNA; 306 BP.						
XX	AAS99530;						
AC							
XX							
DT	12-MAR-2002 (first entry)						
DE	Mycobacterium species identification primer #5.						
XX							
KW	Drug resistance detection; mycobacterial species identification; probe;						
KM	oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;						
KX	primer.						
OS	Mycobacterium bovis.						
PN	WO200192573-AI.						
PD	06-DEC-2001.						
PF	30-MAY-2001; 2001WO-KR00904.						
PR	30-MAY-2000; 2000KR-0029369.						
PA	(BIOM-) BIOMEDLAB CO LTD.						
PI	Kim H, Kim N, Yoon S, Kim J, Park M;						
DR	WPI; 2002-075472/10.						
PT	Kit for mycobacterial species identification and drug resistance						
PT	detection, has oligonucleotide chip with species identification probe,						
PT	a mycobacterial drug-resistance detection probe, and its contrast group						
PT	probe -						
PS	Disclosure; Page 21; 74pp; English.						
XX							
CC	The invention relates to a diagnostic kit for mycobacterial species						
CC	identification and drug resistance detection comprising an						
CC	oligonucleotide chip including a species identification probe, a						
CC	mycobacterial drug-resistance detection probe, a contrast group probe						
CC	corresponding to each drug resistance detection probe, and a marker for						
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The						
CC	identification probe is comprised of species-specific DNA sequences of						
CC	mycobacterial rpoB gene and the detection probe is comprised of one or						
CC	more modified codons of mycobacterial rpoB gene. The method involves						
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction						
CC	(PCR) and discriminating species by fluorescent intensity corresponding						
CC	to a particular species. The specimen is preferably uncultured sputum,						
CC	blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569						
CC	represent mycobacterium species identification probes and primers of the						
CC	invention.						

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20
|||||
Db 5 tacggtcgcgcgagctgattcc 24

RESULT 11

AAS99531
ID AAS99531 standard; DNA; 306 BP.

AC AAS99531;

XX 12-MAR-2002 (first entry)

DE Mycobacterium species identification primer #6.

KW Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;

XX Mycobacterium bovis.

PN WO200192573-A1.

PD 06-DEC-2001.

PF 30-MAY-2001; 2001WO-KR00904.

PR 30-MAY-2000; 2000KR-0029369.

PA (BIOM-) BIOMEDLAB CO LTD.

PI Kim H, Kim N, Yoon S, Kim J, Park M;

DR WPI; 2002-075472/10.

PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -

PS Disclosure; Page 21; 74pp; English.

XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20
|||||
Db 5 tacggtcgcgcgagctgattcc 24

RESULT 12

AA061457
ID AA061457 standard; DNA; 432 BP.

AC AA061457;

DT 17-MAY-1994 (first entry)

DE M. tuberculosis rpoB gene fragment.

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.

OS Mycobacterium tuberculosis.

PN WO9322454-A.

PD 11-NOV-1993.

PF 30-APR-1993; 93WO-EP01063.

PR 17-SEP-1992; 92FR-0011098.

PR 30-APR-1992; 92US-0875940.

PR 14-AUG-1992; 92US-0929206.

PR 16-APR-1993; 93FR-0004545.

PA (ASSI-) ASSISTANCE PUBLIQUE.

PA (INSP) INST PASTEUR.

PA (MED-) MEDICAL RES COUNCIL.

PA (UTBE-) UNIT BERNE.

PA (UTBE-) UNIT CURIE PARIS VI P & M.

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

PI Young D, Zhang Y;

DR WPI; 1993-368812/46.

DR P-PSDB; AAR51372.

XX Rapid detection of antibiotic resistance in Mycobacteria - esp.

PT isoniazid, rifampicin or streptomycin resistance in tuberculosis

PT by detecting mutation in katG, rpoB or rpsL genes

XX Example 2; Fig 13; 97pp; English.

XX PCR amplification was used to obtain rpoB genes from rifampicin-

CC resistant Mycobacterium lepreae strains. A comparison with the

CC sequence of the rpoB gene from sensitive strains (AA051532) revealed

CC mutations in the region encoding amino acids 400-450. The corresp.

CC region was isolated from M. tuberculosis (AA061457). A common

CC mutation seen in resistant strains occurs at codon 425 where Ser is

CC substituted, most frequently by Leu.

SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20

```
Db      18 tacggtcgcgcgcgtatcc 37
|||||
RESULT  13
AAAA9863
ID      AAA49863 standard; DNA; 480 BP.
XX
AC      AAA49863;
XX
DT      25-SEP-2000 (first entry)
XX
DE      Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW      Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS      Mycobacterium tuberculosis.
XX
Key      Location/Qualifiers
FH      primer_bind
FT      complement(41..60)
FT      /tag= a
FT      /note= "primer of AAA49823"
FT      primer_bind
FT      372..391
FT      /tag= b
FT      /note= "primer of AAA49824"
XX
PN      WO200036142-A1.
XX
PD      22-JUN-2000.
XX
PF      10-DEC-1999; 99WO-CA01177.
XX
PR      11-DEC-1998; 98US-0111794.
XX
PA      (VIST-) VISIBLE GENETICS INC.
XX
PI      Shipman R;
XX
DR      WPI: 2000-431611/37.
XX
PT      Method for the detection and characterization of Mycobacterium
PS      tuberculosis with antibiotic resistance in a sample.
XX
PS      Disclosure: Page 5; 43pp; English.
XX
CC      The present sequence is that of the Mycobacterium tuberculosis
CC      rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC      cycle sequencing primers (see AAA49823-62) are used for the detection
CC      and analysis of antibiotic resistance-associated mutations in
CC      defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC      (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC      (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC      (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC      These primers can be used in a method for the detection and
CC      characterization of M. tuberculosis present in a sputum sample.
CC      The method involves performing a sequencing procedure, with or
CC      without prior amplification, to detect the presence of M.
CC      tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC      and 23S genes for the presence of antibiotic-inducing mutations.
CC      If M. tuberculosis is detected, a second sequencing procedure is
CC      performed on the sample to evaluate additional genes for the
CC      presence of antibiotic resistance-inducing mutations. Genotypic
CC      tests are rapid, sensitive and accurate providing information as to
CC      antibiotic treatment options.
XX
SQ      Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
Query Match      100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      41 tacggtcgcgcgcgtatcc 60
|||||
RESULT  14
AAT09676
ID      AAT09676 standard; DNA; 970 BP.
XX
AC      AAT09676;
XX
DT      15-OCT-1996 (first entry)
XX
DE      Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW      Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
XX      polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS      Mycobacterium tuberculosis.
XX
Key      Location/Qualifiers
FH      primer_bind
FT      10..27
FT      /tag= a
FT      /note= "primer FENLFF"
FT      primer_bind
FT      226..243
FT      /tag= b
FT      /note= "primer DDIDHL"
FT      primer_bind
FT      226..240
FT      /tag= c
FT      /note= "primer DDIDH"
FT      primer_bind
FT      338..364
FT      /tag= d
FT      /note= "primer rpo95"
FT      primer_bind
FT      348..373
FT      /tag= e
FT      /note= "primer rpo105"
FT      primer_bind
FT      354..373
FT      /tag= f
FT      /note= "primer KY290"
FT      misc-feature
FT      372..373
FT      /tag= g
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      433..434
FT      /tag= h
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      438
FT      /tag= i
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      468..469
FT      /tag= j
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      486
FT      /tag= k
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      501
FT      /tag= l
FT      /note= "M. tuberculosis signature nucleotide"
FT      misc-feature
FT      516
FT      /tag= m
FT      /note= "M. tuberculosis signature nucleotide"
FT      primer_bind
FT      516..535
FT      /tag= n
FT      /note= "primer rpo273"
FT      misc-feature
FT      525
FT      /tag= o
FT      /note= "M. tuberculosis signature nucleotide"
FT      primer_bind
FT      525..541
FT      /tag= p
FT      /note= "primer KY292"
FT      primer_bind
FT      536..562
FT      /tag= q
FT      /note= "primer rpo293"
FT      primer_bind
FT      640..666
FT      /tag= r
```

```

FT      primer_bind      /note="primer ip0397"
FT      primer_bind      952..966
FT      primer_bind      /*tag= s
FT      primer_bind      /note="primer NMQRQ-1"
FT      primer_bind      952..966
FT      primer_bind      /*tag= t
FT      primer_bind      /note="primer NMQRQ-2"
XX
XX      WO9533074-A1.
XX
XX      07-DEC-1995.
XX
XX      26-MAY-1995. 95MO-US06790.
XX
XX      26-MAY-1994. 94US-0250030.
XX
XX      (HOFF ) HOFFMANN LA ROCHE INC.
XX      (MAYO-) MAYO FOUNDATION.
XX
XX      Felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX      Young KKY;
XX      WPI; 1996-030581/03.
XX
XX      Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX      with a primer set that targets portions of the gene encoding rpoB.
XX      Disclosure: Fig.3; 54pp; English.
XX
XX      This oligonucleotide DNA primer is specific for Mycobacterium
XX      tuberculosis, and may be used to amplify a sample DNA by targeting
XX      a portion of the gene encoding rpoB. The 1st several bases comprise a
XX      nonhybridizing tail consisting of filler bases followed by the
XX      a restriction site incorporated to facilitate cloning using the
XX      amplicon at a later date, if desired. The remaining bases hybridize
XX      to bacterial rpoB DNA. The method provides for the detection of M.
XX      tuberculosis and the concurrent determination of its drug
XX      susceptibility, particularly to rifampin. The method can provide
XX      often greater than 95% sensitivity and 100% specificity. The
XX      biological sample is a fluid or tissue sample from a human.
XX
XX      Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
XX
XX      Query Match      100.0%; Score 20; DB 17; Length 970;
XX      Best Local Similarity 100.0%; Pred. No. 1.6;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 tacggtcgcgcgagctgattcc 20
XX      Db      261 tacggtcgcgcgagctgattcc 280
XX
XX      RESULT 15
XX      AAH51976
XX      ID AAH51976 standard; DNA; 3519 BP.
XX
XX      AAH51976;
XX
XX      04-SEP-2001 (first entry)
XX
XX      Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX      Drug target; growth; organism viability; characterisation; ds.
XX
XX      Mycobacterium tuberculosis.
XX
XX      WO200135317-A1.
XX
XX      17-MAY-2001.
XX
XX      13-NOV-2000; 2000WO-US31152.
XX

```

```

PR      12-NOV-1999; 99US-0165086.
PR      12-NOV-1999; 99US-0165124.
PR      01-FEB-2000; 2000US-0179531.
XX
XX      (REGC ) UNIV CALIFORNIA.
XX
XX      Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX      WPI; 2001-329193/34.
XX      P-PSDB; AAG81125.
XX
XX      Identifying nucleotide or polypeptide sequence for use as drug target,
XX      involves providing algorithm that analyzes a functional relationship
XX      between nucleotide or polypeptide sequences, and comparing the
XX      sequences
XX
XX      Disclosure; Page 68-69; 207pp; English.
XX
XX      This invention relates to a method for identifying a nucleotide or
XX      polypeptide sequence that may be a drug target, or essential for growth
XX      or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX      represent DNA encoding proteins AAG81096 - AAG81241. Mycobacterium
XX      tuberculosis proteins which are potential drug targets. The DNA and
XX      protein sequences are used to illustrate the method of the invention. The
XX      method involves providing an unknown nucleotide or polypeptide sequence,
XX      and comparing it to a number of sequences along with at least one
XX      algorithm capable of analysing a functional relationship between
XX      nucleotide and polypeptide sequences. The method is useful for
XX      characterising the function of nucleic acids and polypeptides that may be
XX      useful as a target for a drug or essential for the growth or viability of
XX      an organism.
XX
XX      Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX      Query Match      100.0%; Score 20; DB 22; Length 3519;
XX      Best Local Similarity 100.0%; Pred. No. 1.6;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 tacggtcgcgcgagctgattcc 20
XX      Db      1119 tacggtcgcgcgagctgattcc 1138
XX

```

Search completed: August 7, 2002, 22:04:01
Job time: 8061 sec

This Page Blank (uspto)

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgccgagctgattcc 20
|||||
Db 1 tacgctcgccgagctgattcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823;
XX

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KM ss.

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgccgagctgattcc 20
|||||
Db 1 tacgctcgccgagctgattcc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825;
XX

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcgagctgacc 20
Db 1 tacggtcggcgagctgacc 20
|||||

RESULT 4
AAx27214
ID AAX27214 standard; DNA: 306 BP.
XX
XX AAX27214;
XX
XX 27-MAY-1999 (first entry)
XX
XX
DE RpoB gene fragment.
XX
XX RpoB gene: mycobacteria; phylogenetic tree construction;
XX mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria tuberculosis.
XX
XX W09905316-A1.
XX
XX 04-FEB-1999.
XX
XX 28-JUL-1998; 98KR-0000228.
XX
XX 28-JUL-1997; 97KR-0035501.
XX
XX (BION-) BIONEER CORP.
XX
XX Kim B, Kook Y;
XX
XX WPI; 1998-539367/46.
XX
XX
XX New pair of polymerase chain reaction (PCR) primers - for
XX sequence-specific amplification of the rpoB gene from mycobacterial
XX species, useful for detecting and identifying mycobacterial species
XX
XX Claim 43; Page 75-76; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
XX amplified using the PCR primers of the invention. The primers form a
XX method of detecting and identifying mycobacterial species by constructing
XX a phylogenetic tree for the species. The use of the primers for
XX sequence-specific amplification of the rpoB gene (encoding the beta
XX subunit of RNA polymerase) from mycobacterial species provides an
XX efficient way of characterising these species. In addition to
XX phylogenetic analysis, the rpoB gene can be used as an alternative to
XX the 16S rRNA gene because it has four subunits, which are highly
XX conserved throughout prokaryotes. The method is particularly useful for
XX slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
XX susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcgagctgacc 20
Db 5 tacggtcggcgagctgacc 24
|||||

RESULT 5
AAX27175
ID AAX27175 standard; DNA: 306 BP.
XX
XX AAX27175;
XX
XX 27-MAY-1999 (first entry)
XX
XX
DE RpoB gene fragment.
XX
XX RpoB gene: mycobacteria; phylogenetic tree construction;
XX mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria africanum.
XX
XX W09905316-A1.
XX
XX 04-FEB-1999.
XX
XX 28-JUL-1998; 98KR-0000228.
XX
XX 28-JUL-1997; 97KR-0035501.
XX
XX (BION-) BIONEER CORP.
XX
XX Kim B, Kook Y;
XX
XX WPI; 1998-539367/46.
XX
XX
XX New pair of polymerase chain reaction (PCR) primers - for
XX sequence-specific amplification of the rpoB gene from mycobacterial
XX species, useful for detecting and identifying mycobacterial species
XX
XX Claim 4; Page 62-63; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
XX amplified using the PCR primers of the invention. The primers form a
XX method of detecting and identifying mycobacterial species by constructing
XX a phylogenetic tree for the species. The use of the primers for
XX sequence-specific amplification of the rpoB gene (encoding the beta
XX subunit of RNA polymerase) from mycobacterial species provides an
XX efficient way of characterising these species. In addition to
XX phylogenetic analysis, the rpoB gene can be used as an alternative to
XX the 16S rRNA gene because it has four subunits, which are highly
XX conserved throughout prokaryotes. The method is particularly useful for
XX slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
XX susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcgagctgacc 20
Db 5 tacggtcggcgagctgacc 24
|||||

RESULT 6
AAX27179

```

ID  AAX27179 standard; DNA; 306 BP.
XX
XX  AAX27179:
AC
XX  27-MAY-1999 (first entry)
DT
XX  RPOB gene fragment.
DE
XX  RPOB gene: mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX  Mycobacteria bovis.
OS
XX  WO9905316-A1.
PN
XX  04-FEB-1999.
PD
XX  28-JUL-1998; 98KR-0000228.
PF
XX  28-JUL-1997; 97KR-0035501.
PR
XX  (BION-) BIONEER CORP.
PA
XX  Kim B, Kook Y;
PI
XX  WPI; 1998-539367/46.
DR
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
PS  Claim 8; Page 64; 91pp; English.
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
CC
XX  Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ

```

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY  1 tacggtcgcgagctgac 20
    |||
Db  5 tacggtcgcgagctgac 24

```

RESULT 7
AAX27180
ID AAX27180 standard; DNA; 306 BP.
XX
XX AAX27180:
AC
XX 27-MAY-1999 (first entry)
DT
XX RPOB gene fragment.
DE
XX RPOB gene: mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX Mycobacteria bovis.
OS
XX

```

PN  WO9905316-A1.
XX
XX  04-FEB-1999.
PD
XX  28-JUL-1998; 98KR-0000228.
PF
XX  28-JUL-1997; 97KR-0035501.
PR
XX  (BION-) BIONEER CORP.
PA
XX  Kim B, Kook Y;
PI
XX  WPI; 1998-539367/46.
DR
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
PS  Claim 9; Page 64; 91pp; English.
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
CC
XX  Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

```

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY  1 tacggtcgcgagctgac 20
    |||
Db  5 tacggtcgcgagctgac 24

```

RESULT 8
AAS99526
ID AAS99526 standard; DNA; 306 BP.
XX
XX AAS99526:
AC
XX 12-MAR-2002 (first entry)
DT
XX Mycobacterium species identification primer #1.
DE
XX Mycobacterium tuberculosis.
OS
XX Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.
XX Mycobacterium tuberculosis.
OS
XX WO200192573-A1.
PN
XX 06-DEC-2001.
PD
XX 30-MAY-2001; 2001WO-KR00904.
PF
XX 30-MAY-2000; 2000KR-0029369.
PR
XX (BION-) BIOMEDLAB CO LTD.
PA
XX Kim H, Kim N, Yoon S, Kim J, Park M;
XX

DR	WPI; 2002-075472/10.
XX	
PT	Kit for mycobacterial species identification and drug resistance
PT	detection, has oligonucleotide chip with species identification probe,
PT	a mycobacterial drug-resistance detection probe, and its contrast group
PT	probe -
XX	
PS	Disclosure; Page 21; 74pp; English.
XX	
CC	The invention relates to a diagnostic kit for mycobacterial species
CC	identification and drug resistance detection comprising an
CC	oligonucleotide chip including a species identification probe, a
CC	mycobacterial drug-resistance detection probe, a contrast group probe
CC	corresponding to each drug resistance detection probe, and a marker for
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC	identification probe is comprised of species-specific DNA sequences of
CC	mycobacterial rpoB gene and the detection probe is comprised of one or
CC	more modified codons of mycobacterial rpoB gene. The method involves
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC	(PCR) and discriminating species by fluorescent intensity corresponding
CC	to a particular species. The specimen is preferably uncultured sputum,
CC	blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC	represent mycobacterium species identification probes and primers of the
CC	invention.
XX	
SQ	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
Query Match	100.0%; Score 20; DB 24; Length 306;
Best Local Similarity	100.0%; Pred. NO. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DY	1 tacggtcgcgcagctcatcc 20
Db	5 tacggtcgcgcagctcatcc 24
RESULT 9	
AAS99527	
ID	AAS99527 standard; DNA; 306 BP.
XX	
AC	AAS99527;
XX	
DT	12-MAR-2002 (first entry)
DE	Mycobacterium species identification primer #2.
XX	
KM	Drug resistance detection; mycobacterial species identification; probe;
KW	oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW	primer.
XX	
OS	Mycobacterium africanum.
NX	
NN	WO200192573-A1.
PD	
PD	06-DEC-2001.
XX	
PE	30-MAY-2001; 2001WO-KR00904.
XX	
PR	30-MAY-2000; 2000KR-0029369.
XX	
PA	(BIOM-) BIOMEDLAB CO LTD.
XX	
PI	Kim H, Kim N, Yoon S, Kim J, Park M;
DR	WPI; 2002-075472/10.
XX	
PT	Kit for mycobacterial species identification and drug resistance
PT	detection, has oligonucleotide chip with species identification probe,
PT	a mycobacterial drug-resistance detection probe, and its contrast group
PT	probe -
XX	
NS	Disclosure; Page 21; 74pp; English.

The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium species identification probes and primers of the invention.

Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 1 tacgagtcggcgaagctgatcc 20
 |||||||
Db 5 tacggtcgcgagctgatcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
OS Mycobacterium bovis.
PN WO200192573-A1.
PD 06-DEC-2001.
PF 30-MAY-2001; 2001WO-KR00904.
PR 30-MAY-2000; 2000KR-0029369.
RA (BIOM-) BIOMEDLAB CO LTD.
RI Kim H, Kim N, Yoon S, Kim J, Park M;
WP1: 2002-075472/10.
The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other:

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcagctgatcc 20
|||||
5 tacggtcgagcagctgatcc 24

Db

RESULT 11
AAS99531
ID AAS99531 standard; DNA; 306 BP.
XX
AC AAS99531;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #6.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.

XX
OS Mycobacterium bovis.
XX
PN W0200192573-A1.
XX
PD 06-DEC-2001.
XX
PE 30-MAY-2001; 2001MO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
PT kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -

XX
PS Disclosure; Page 21; 74pp; English.

XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other:

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcagctgatcc 20
|||||
5 tacggtcgagcagctgatcc 24

Db

RESULT 12
AA061457
ID AA061457 standard; DNA; 432 BP.
XX
AC AA061457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M. tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN W09322454-A.
XX
PD 11-NOV-1993.
XX
PE 30-APR-1993; 93MO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
XX
PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes

XX
PS Example 2; Fig 13; 97pp; English.

XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M. tuberculosis (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.

XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other:

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcagctgatcc 20


```

FT      primer_bind /note= "primer rpo397"
FT      primer_bind /tag= S
FT      primer_bind /note= "primer NMORQ-1"
FT      primer_bind /tag= t
FT      primer_bind /note= "primer NMORQ-2"
PN      MO9533074-A1.
XX
XX      07-DEC-1995.
XX
XX      26-MAY-1995; 95WO-US06790.
XX
XX      26-MAY-1994; 94US-0250030.
XX
XX      (HOFF ) HOFFMANN LA ROCHE INC.
XX      (MAYO-) MAYO FOUNDATION.
XX
XX      Felmelee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX      Young KKY;
XX      WPI; 1996-030581/03.
XX
XX      Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX      with a primer set that targets portions of the gene encoding rpoB.
XX      Disclosure; Fig.3; 54pp; English.
XX
XX      This oligonucleotide DNA primer is specific for Mycobacterium
XX      tuberculosis, and may be used to amplify a sample DNA by targeting
XX      a portion of the gene encoding rpoB. The 1st several bases comprise a
XX      nonhybridizing tail consisting of filler bases followed by
XX      a restriction site incorporated to facilitate cloning using the
XX      amplicon at a later date, if desired. The remaining bases hybridize
XX      to bacterial rpoB DNA. The method provides for the detection of M.
XX      tuberculosis and the concurrent determination of its drug
XX      susceptibility, particularly to rifampin. The method can provide
XX      often greater than 95% sensitivity and 100% specificity. The
XX      biological sample is a fluid or tissue sample from a human.
XX
XX      Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcagctgctacc 20
Db 261 tacggtcgcgcagctgctacc 280

RESULT 15
AAH51976
ID AAH51976 standard; DNA; 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US31152.
XX

```

```

PR      12-NOV-1999; 99US-0165086.
PR      12-NOV-1999; 99US-0165124.
PR      01-FEB-2000; 2000US-0179531.
XX
XX      (REGC ) UNIV CALIFORNIA.
XX
XX      Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX      WPI; 2001-329193/34.
XX      P-PSDB; AAG81125.
XX
XX      Identifying nucleotide or polypeptide sequence for use as drug target,
XX      involves providing algorithm that analyzes a functional relationship
XX      between nucleotide or polypeptide sequences, and comparing the
XX      sequences.
XX
XX      Disclosure; Page 68-69; 207pp; English.
XX
XX      This invention relates to a method for identifying a nucleotide or
XX      polypeptide sequence that may be a drug target, or essential for growth
XX      or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX      represent DNA encoding proteins AAG81096 - AAG81241. Mycobacterium
XX      tuberculosis proteins which are potential drug targets. The DNA and
XX      protein sequences are used to illustrate the method of the invention. The
XX      method involves providing an unknown nucleotide or polypeptide sequences,
XX      and comparing it to a number of sequences along with at least one
XX      algorithm capable of analysing a functional relationship between
XX      nucleotide and polypeptide sequences. The method is useful for
XX      characterising the function of nucleic acids and polypeptides that may be
XX      useful as a target for a drug or essential for the growth or viability of
XX      an organism.
XX
XX      Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcagctgctacc 20
Db 1119 tacggtcgcgcagctgctacc 1138

```

Search completed: August 7, 2002, 22:03:58
Job time: 8058 sec

translation="MLDVNFDELRLIGLATADIROMSYGEVKKPETINRYRLKPEKD
GLECEKIFGPTDMECYCGKRYKRGKGIICERCGEVTRAKYRERMHIEIAAPVT
HIMYFKGVSRLGIYLLDAPKDEKTIYFAAVITSVDEMRHNL"
BASE COUNT 969 a 1534 c 1691 g 890 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacgagcgttcgatagaacc 20
|||||
Db 2611 TACGGCGTTGATGACCC 2592
RESULT 15
AE006964 19352 bp DNA linear BCF 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
DEFINITION complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
1 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
JOURNAL
Unpublished
2 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE
Direct Submission
JOURNAL
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
FEATURES
SOURCE
Location/Organism
1. 19352
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
/db_xref="taxon:83331"
/note="clinical strain"
163. 3699
/gene="MT0695"
163. 3699
/gene="MT0695"
/note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
PID:149992. Identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK44921.1"
/db_xref="GI:13880218"
/translation="MLBGCILADRSKSTASPSRROSSNNNSVGPAPRVAFRL
REPLEVEGLDVOITDFEMLIGSPRMRSAERGDVNPVGLELYLELSIEDPSSG
MSLSFSDPRDVAAPVDECKDMDTYAAPLEVAEILNNVTGKISGVAMGEPMM
TEKCTFLINTEVERVAVSOLVSPGVYEDETIDKSTDKLHSVKVIPSAGALDEVDK
RDVAVRIDRRQRPVYLKALCMTSEQIVSEIGSEIMRSTLEKIDNTVGTDEALD
IYRLRGDEPTKSAOTLLENLFKEKRYDLAVRGYKVKKLGKLGHWGEPITSSTL
EDVYATLEYLVRLEHGTMTVPGVGEVPEVETDIDHGNRLRTVELONPLIRG
MSMRVYREKMTTODVAITPQILINIRPVAAIKFEFGTSQSLQDFDNPNISGLT
HKRLISALPGSLSRERAGLEVDPVHPSHGRMCPETPEGNIGLIGLSIVYRVNP

gene
CDS
3744. 7694
/gene="MT0696"
/note="similar to SP:P37871; identified by sequence
similarity; putative"
/transl_table=1
/codon_start=1
/product="DNA-directed RNA polymerase, beta-prime subunit"
/protein_id="AAK44922.1"
/db_xref="GI:13880219"
/translation="MLDVNFDELRLIGLATADIROMSYGEVKKPETINRYRLKPEKD
GLCEKIFGPTDMECYCGKRYKRGKGIICERCGEVTRAKYRERMHIEIAAPVT
HIMYFKGVSRLGIYLLDAPKDEKTIYFAAVITSVDEMRHNLSTAEAVERK
AVDORGELEAROKLEADLEAAGARARVARDGEREMQIRORAEIDR
LEDIMSTFKLAPKOLIVDENLYRELVDYRGFTGMAGSESLOKLENDIDIAEAS
LRDVIYRNGKOKKRLALKVVAAPFOOSGNSPMGDMAPVPIPELRPMVLDGGR
FATSDLDLYLRVYINRNRLKRLIDGAPETIYNKEMKESVDLFDNGRGPAT
GPGKRLPLKSLDKOGFRONLCKRQVDSGRSYIYVGPOLKHOGLKPLMALE
LFRPEVKRLVLDLHNAONISAKRWERORPQVWDVLEVIABEVLNKAAPTLHRG
IOAFEPMLVEGKALIOHPLVCEAFNADPDDONAHLPLSAEOAERILMLSSNLT
SPASGRPLARLDIMVHGLYLTETVEDEGEOPASGDPETVGSSPAEALMAOR
GVSIVRAKIVYRLOLRPAVEIEALEVAGVMDKMGQDMAMETLGRVFNELPLGVP
FVNKMKKVOAALINDLAREPVIYAVGVNDKDGFWAATRSVGMADVLVPE
RKKEIDHYERADRVKORQALNNDENALVEYKSKSPREGVLVLEFPITRHA
ITIVDSGATGNFTOTRLAGMGLVNPVNGEETPRVXSSPREGVLVLEFPITRHA
RKLADPALRTADSGYLTRLVDSOVIVREHCCOTERGIIVELARABDGLITRIP
YIETSAFARTLGTDAVDAGNVIVEROGDIDALMLAAGITOVVRVLCANST
GYCATGYSRMAKTLVDIGAVGIVVAOSIGERGQTLTRTFHOGGVDIGSLPR
VOELFEARVPRKAPIDAVTGRVLEEGERYKLTIVPDGGEVVDKISKROLRV
FKHEDSERVLSDGDHYEQOLMEGSADEPVEVIRNGPREVOHILVREOVYRAG
VSHDKHIEVYRMLKRVTLIDSGSTFPLGSLDAEAEAKRRVYASGGERAAR
PVLMDGITKASLATDSMLASAFQETTVLTDAALNCSDKLNGKLEKENVITGLIPACT
GINRYRNAVOPTEEARAAATTPSYEDQYVSPDGAATGAALVDYGVSDYR"
complement(7691..8065)
/gene="MT0697"
complement(7691..8065)
/gene="MT0697"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK44923.1"
/db_xref="GI:13880220"
/translation="MFDAAATNPGHAMASAMERSGLLECVAQLDQPEGTADKL
NPDRGSRVPRROADGILTHVERGGORSGOAGVQVPRMGFPALAMQDRLLHH
GEORNRITAOAFRVFCVSPY"
complement(8058..9972)
/gene="MT0698"
/note="this region contains an authentic frame shift and
is not the result of a sequencing artifact; identified by
Glimmer2; putative; conserved hypothetical protein,
authentic frameshift"
10167. 10925
/gene="MT0699"
10167. 10925
/gene="MT0699"
/note="identified by match to PFAM protein family HM
PF01261"
/codon_start=1
/transl_table=1

Query Match 100.0% Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 1547 TACGGCGTTTCGATGAACCC 1528

RESULT 13
LOCUS MTU12205

DEFINITION Mycobacterium tuberculosis H37Rv RNA polymerase beta subunit (rpoB)
gene, partial cds.

ACCESSION U12205
VERSION U12205.1 GI:515684

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

gene
CDS

1.3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..3853
/gene="rpoB"
576..3853
/gene="rpoB"
/codon_start=1
/transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="AAA20242.2"
/translation="MEEGCIADSRKSTAAASPSRPOSSNNNSVPGAPNRYSAKL
REPLEVPGCLDVQDSFEMLTGSPRMRSAERGDVNPVGGLEVLIELSPIDFSGS
MSLSPDRFDVKAAPVDECKDKDMTAAFLVTAETINNNGEIKSQVFMGDFPM
TEKGFITINGTERVAVVSOVLRSPGVFDETDIKSTDKTLHSVKVIPSFGAMLEFDVK
RDYGVRLDRKRQRPVTVLLKALGMTSEQIVFERGSEIMRSTLEKNTVGTDEALLD
IRKLRGEPPTKESAOITLLENLFKEKRYDLARVGRYKNNKLGILGVGRTSTLT
EDVVAITIEYLVRHEGQTTWVPGVEVPEETDIDHFGNRLRTVGETLQNIQIRG
MSRMRYVERMTTQDVEAITPOTLINIRPVAAIKFEPTSQLSQDQNNPLSGLT
HKRRISALGPGSLRERAGLEVDRVSHSGKCPITPEGPNIIGLISVAVRNP
EGFLETPEYRKVGVSDGYLYLDAEDRHVVAQANSPIDAGREVEPVILVRKAG
EVEYVSSVDVMDVSPROMSVATAPIPLEHDDANRALGAMMOQAVPLVRKAP
LVGTGMELRADIAATSSQSGVIEVSADYITVMHNDGTRTYRRKFRANSNGTC
ANOCPIVADGADREAGVVIADGCTDGEALGKMLVAIMEGHNYDAITLSRL
VEEDVLTSHIEHEIDARDTKLGAETIRDPINISDEVIALDDEGTYRIGAEVSDG
DILVGVKTPKGETELPEERLRALFGKAEIRVDSKYPHESGRTVIGIRFVSRED
EDELPAVGNELVRYVAVOKRKISDGKLAGRHGNKAVIGKILFVEDMPFLADGTPVDI
TLPVTDGAQEAELDGLSCTLPNRDGVILVDADGKAMLPDGRSGEPPTVPTGYMIM
TKHLVDDKTHARSTGPTSMITQOPLGKAQFGGFRGMECMAMQAYGAATLTQIELL
TIKS"

BASE COUNT
ORIGIN

723 a 1173 c 1293 g 664 t

Query Match 100.0% Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 14
LOCUS MSGRPOB/c

DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
gene, complete cds and RNA polymerase beta-subunit rpoC gene,
partial cds.

ACCESSION L27989.1 GI:468333

VERSION L27989

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

gene
CDS

1.5084
Location/Qualifiers
/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"
1065..4598
/gene="rpoB"
1065..4598
/gene="rpoB"
/codon_start=1
/transl_table=11
/evidence=experimental
/product="RNA polymerase beta-subunit"
/protein_id="AAA21416.1"
/db_xref="GI:468334"
/translation="MEEGCIADSRKSTAAASPSRPOSSNNNSVPGAPNRYSAKL
REPLEVPGCLDVQDSFEMLTGSPRMRSAERGDVNPVGGLEVLIELSPIDFSGS
MSLSPDRFDVKAAPVDECKDKDMTAAFLVTAETINNNGEIKSQVFMGDFPM
TEKGFITINGTERVAVVSOVLRSPGVFDETDIKSTDKTLHSVKVIPSFGAMLEFDVK
RDYGVRLDRKRQRPVTVLLKALGMTSEQIVFERGSEIMRSTLEKNTVGTDEALLD
IRKLRGEPPTKESAOITLLENLFKEKRYDLARVGRYKNNKLGILGVGRTSTLT
EDVVAITIEYLVRHEGQTTWVPGVEVPEETDIDHFGNRLRTVGETLQNIQIRG
MSRMRYVERMTTQDVEAITPOTLINIRPVAAIKFEPTSQLSQDQNNPLSGLT
HKRRISALGPGSLRERAGLEVDRVSHSGKCPITPEGPNIIGLISVAVRNP
EGFLETPEYRKVGVSDGYLYLDAEDRHVVAQANSPIDAGREVEPVILVRKAP
LVGTGMELRADIAATSSQSGVIEVSADYITVMHNDGTRTYRRKFRANSNGTC
ANOCPIVADGADREAGVVIADGCTDGEALGKMLVAIMEGHNYDAITLSRL
VEEDVLTSHIEHEIDARDTKLGAETIRDPINISDEVIALDDEGTYRIGAEVSDG
DILVGVKTPKGETELPEERLRALFGKAEIRVDSKYPHESGRTVIGIRFVSRED
EDELPAVGNELVRYVAVOKRKISDGKLAGRHGNKAVIGKILFVEDMPFLADGTPVDI
TLPVTDGAQEAELDGLSCTLPNRDGVILVDADGKAMLPDGRSGEPPTVPTGYMIM
TKHLVDDKTHARSTGPTSMITQOPLGKAQFGGFRGMECMAMQAYGAATLTQIELL
REGEDEDELRANALGINTLSNSESFEDELA"
/gene="rpoC"
4641..5084
/gene="rpoC"
/gene="rpoC"
/codon_start=1
/transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:537608"

partial cds.
 AF060353
 VERSION AF060353.1 GI:3133464
 KEYWORDS
 SOURCE Mycobacterium tuberculosis.
 ORGANISM Mycobacterium tuberculosis.
 Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium tuberculosis complex.
 1 (bases 1 to 705)
 AUTHORS Gingeras, T.R., Ghandour, G., Wang, E., Bero, A., Small, P.M.,
 Drobniewski, F., Alland, D., Desmond, E., Holodny, M., and Drenkow, J.
 TITLE Simultaneous genotyping and species identification using
 hybridization pattern recognition analysis of generic mycobacterium
 DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 MEDLINE 98248685
 REFERENCE 2 (bases 1 to 705)
 AUTHORS Gingeras, T.R., Ghandour, G., Wang, E., Bero, A., Small, P.M.,
 Drobniewski, F., Alland, D., Desmond, E., Holodny, M., and Drenkow, J.
 TITLE Direct Submission
 JOURNAL Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
 380 Central Expressway, Santa Clara, CA 95051, USA
 FEATURES
 source
 1. 705
 /organism="Mycobacterium tuberculosis"
 /strain="ATCC27294"
 /db_xref="ATCC:27294"
 /db_xref="taxon:1773"
 <1. >705
 /gene="rpoB"
 <1. >705
 /gene="rpoB"
 /codon_start=3
 /transl_table=11
 /product="RNA polymerase beta-subunit"
 /protein_id="AAC38533.1"
 /db_xref="GI:3133465"
 /translation="QDEAITPQTLNIRPVVAIKFEFTSOLQFMDONPLSGLT
 HKRRLSLGPGSLSRERAGLEVRDHSYHGRCPTPGSPNGLIGSLSVARVP
 FGRTERPYRVGVGCVSDERYLYLTADDEDDHVAQANSPIDAGREYEPVLRKAG
 EYEVPSSEVDYNDVSPROMSVATNATIPLEHDDANRALMGANMQAVPLVASEAP
 LVGTGMLRAITDAAT"
 BASE COUNT 117 a 227 c 250 g 111 t
 ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 705;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 ||||||||||||||||||
 DB 331 TACGGCGTTTCGATGAACCC 312

RESULT 10
 ARI49128/c 706 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI49128
 DEFINITION Sequence 24 from patent US 6228575.
 ACCESSION ARI49128
 VERSION ARI49128.1 GI:15113719
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 706)
 AUTHORS Gingeras, T.R., Mack, D., Chee, M.S., Bero, A.J., Stryer, L.,
 Ghandour, G., and Wang, C.
 TITLE Chip-based species identification and phenotypic characterization
 of microorganisms
 JOURNAL Patent: US 6228575-A 24 08-MAY-2001;
 FEATURES Location/Qualifiers

source 1. 706
 BASE COUNT 117 a 227 c 250 g 111 t 1 others
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 ||||||||||||||||||
 DB 332 TACGGCGTTTCGATGAACCC 313

RESULT 11
 150706/c 970 bp DNA linear PAT 07-OCT-1997
 LOCUS 150706
 DEFINITION Sequence 1 from patent US 5643723.
 ACCESSION 150706
 VERSION 150706.1 GI:2472409
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 970)
 AUTHORS Persing, D.H., Hunt, J.J., Young, K.K.Y., Fejmlee, T.A., Roberts, G.D.,
 and Whelan, A. Christian.
 TITLE Detection of a genetic locus encoding resistance to rifampin in
 mycobacterial cultures and in clinical specimens
 JOURNAL Patent: US 5643723-A 1 01-JUL-1997;
 FEATURES Location/Qualifiers
 source
 1. 970
 /organism="unknown"
 BASE COUNT 182 a 302 c 330 g 156 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 ||||||||||||||||||
 DB 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
 AX111339/c 3534 bp DNA linear PAT 30-APR-2001
 LOCUS AX111339
 DEFINITION Sequence 2072 from Patent WO0123604.
 ACCESSION AX111339
 VERSION AX111339.1 GI:13927631
 KEYWORDS
 SOURCE Mycobacterium tuberculosis.
 ORGANISM Mycobacterium tuberculosis.
 Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium tuberculosis complex.
 1 (bases 1 to 3534)
 AUTHORS Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
 Picard, F.J., and Roy, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 for detection of microorganisms
 JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source
 1. 3534
 /organism="Mycobacterium tuberculosis"
 /strain="Rv"
 /db_xref="taxon:1773"
 BASE COUNT 679 a 1081 c 1188 g 586 t
 ORIGIN

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c
LOCUS AR062058 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 137 from patent US 5843669.
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059
LOCUS AR062059 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 138 from patent US 5843669.
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060
LOCUS AR062060 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 139 from patent US 5843669.
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061
LOCUS AR062061 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 140 from patent US 5843669.
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c
LOCUS AF060353 705 bp DNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,

CDS
/db_xref="taxon:1773"
<1..>432
/codon_start=1
/transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="AB59068.1"
/db_xref="GI:149992"
/translation="GNRRRTVGEIIONOIRVGSMMERVRERMTTQDEAITPOTL
INTRPVVAIKKEPFGSOLFMDONNPISGLTHKRLSLGPGLSREPAQLEVRDV
HSHYGRMCPTEPECPNIGLISLVSIVARVNPFGTEPYR"
149
/phenotype="rifampicin resistant in association with
mutation 234 G"
188
/replace="c"
/phenotype="rifampicin resistant"
191
/replace="c"
/phenotype="rifampicin resistant in association with
mutation 203 T"
194
/replace="c"
/phenotype="rifampicin resistant"
203
/replace="t"
/phenotype="rifampicin resistant"
208..210
/replace="t"
/phenotype="rifampicin resistant"
232
/replace="a"
/phenotype="rifampicin resistant"
232
/replace="g"
/phenotype="rifampicin resistant"
233
/replace="a"
/phenotype="rifampicin resistant"
233
/replace="g"
/phenotype="rifampicin resistant"
234
/phenotype="rifampicin resistant"
247..248
/replace="g"
/phenotype="rifampicin resistant"
248
/replace="ca"
/phenotype="rifampicin resistant"
248
/replace="g"
/phenotype="rifampicin resistant"
248
/phenotype="rifampicin resistant"
248
/replace="c"
/phenotype="rifampicin resistant"
254
/phenotype="rifampicin resistant"
/replace="c"
BASE COUNT 77 a 140 c 148 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
AR067448/c 432 bp DNA linear PAT 29-SEP-1999
LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
ACCESSION AR067448
VERSION AR067448.1 GI:5998670
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 77 a 139 c 149 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
AR062056/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062056
DEFINITION Sequence 135 from patent US 5843669.
ACCESSION AR062056
VERSION AR062056.1 GI:5989747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT 103 a 202 c 214 g 101 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
AR062057/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062057
DEFINITION Sequence 136 from patent US 5843669.
ACCESSION AR062057
VERSION AR062057.1 GI:5989748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 620)
Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid using thermostable methanococcus
jannaschii FBN-1 endonucleases
Patent: US 5843669-A 135 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:01 ; Search time 2179.67 Seconds

(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-2

Sequence: 1 taagcgcttcgatgaacc 20

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 segs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_em:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
------------	-------	-------	-------	--------	----	----	-------------

C	1	20	100.0	432	1	MSGRIFFNAP	L05910 Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448 Sequence
C	3	20	100.0	620	6	AR062056	AR062056 Sequence
C	4	20	100.0	620	6	AR062057	AR062057 Sequence
C	5	20	100.0	620	6	AR062058	AR062058 Sequence
	6	20	100.0	620	6	AR062059	AR062059 Sequence
	7	20	100.0	620	6	AR062060	AR062060 Sequence
	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AR060353	AR060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	IS0706	IS0706 Sequence
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MTU12205	MTU12205
C	14	20	100.0	5084	1	MSGRPOB	MSGRPOB
C	15	20	100.0	19352	1	AE006964	AE006964
C	16	20	100.0	19770	1	MRC1376	MRC1376
C	17	17	85.0	3316	1	AF172323	AF172323 Bacillus
C	18	15	75.0	27	6	IS0714	IS0714 Sequence
C	19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
C	20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
	21	15	75.0	239050	1	AL596169	AL596169 Listeria
	22	14	70.0	143	3	AF277396	AF277396 Crithidia
	23	14	70.0	409	1	CSPAC228	CSPAC228
	24	14	70.0	442	8	AF080428	AF080428 Agrobacte
	25	14	70.0	458	8	AF080421	AF080421 Agrobacte
	26	14	70.0	518	1	AF325874	AF325874 Agrobacte
	27	14	70.0	762	1	SHEPNTC	SHEPNTC
	28	14	70.0	791	33	AC048639	AC048639 Giardia
	29	14	70.0	1128	8	AB044172	AB044172 Yamagishi
C	30	14	70.0	1194	3	FHEPMDA	FHEPMDA
C	31	14	70.0	1959	8	ATH10B6A	ATH10B6A
C	32	14	70.0	2612	3	FHEPMDA	FHEPMDA
C	33	14	70.0	2615	10	RNPKCETA	RNPKCETA
	34	14	70.0	3218	10	AF146518	AF146518 Rattus no
	35	14	70.0	3240	8	SCU06465	SCU06465 Saccharomyc
C	36	14	70.0	3447	6	AR067447	AR067447 Sequence
	37	14	70.0	3639	10	AF214568	AF214568 Rattus no
	38	14	70.0	4075	10	AF146044	AF146044 Rattus no
	39	14	70.0	4887	3	AF069181	AF069181 Drosophila
	40	14	70.0	6211	3	CEP14A5	CEP14A5
	41	14	70.0	6275	6	AX345453	AX345453 Sequence
	42	14	70.0	6275	6	AX348335	AX348335 Sequence
C	43	14	70.0	9086	1	AE001767	AE001767 Thermotog
	44	14	70.0	9728	6	AX346805	AX346805 Sequence
	45	14	70.0	9728	6	AX348479	AX348479 Sequence

ALIGNMENTS

RESULT 1
MSGRIFFNAP/c
LOCUS
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
SOURCE RNA polymerase beta-subunit; rifampicin resistance.
ORGANISM Mycobacterium tuberculosis (strain H37) DNA.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
Telenti, A., Imboden, P., Marchesi, F., Lowrie, D., Cole, S. T., Colston, J., Matter, L., Schopfer, K. and Bonger, T.
Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 341, 647-650 (1993)
JOURNAL
FEATURES
source
1. 432
/organism="Mycobacterium tuberculosis"
/strain="H37"

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
(without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20

Sequence: 1 tacggtcgcgagctgatcc 20

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	US-08-750-088A-70
2	20	100.0	306	4	US-09-147-935A-2
3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-250-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18.4	92.0	25	4	US-08-750-088A-30
13	18.4	92.0	306	4	US-09-147-935A-4
14	18.4	92.0	306	4	US-09-147-935A-9
15	18.4	92.0	306	4	US-09-147-935A-10
16	18.4	92.0	306	4	US-09-147-935A-20
17	18.4	92.0	306	4	US-09-147-935A-23
18	18.4	92.0	306	4	US-09-147-935A-45
19	17.4	87.0	306	4	US-09-147-935A-13
20	17.4	87.0	306	4	US-09-147-935A-16
21	17.4	87.0	306	4	US-09-147-935A-25
22	17.4	87.0	306	4	US-09-147-935A-31
23	17.4	87.0	306	4	US-09-147-935A-39
24	17.4	87.0	306	4	US-09-147-935A-43
25	17.4	87.0	306	4	US-09-147-935A-46
26	17.4	87.0	306	4	US-09-147-935A-47
27	16.8	84.0	306	4	US-09-147-935A-1

28	16.8	84.0	306	4	US-09-147-935A-8	Sequence 8, Appl
29	15.8	79.0	306	4	US-09-147-935A-5	Sequence 5, Appl
30	15.8	79.0	306	4	US-09-147-935A-12	Sequence 12, Appl
31	15.8	79.0	306	4	US-09-147-935A-14	Sequence 14, Appl
32	15.8	79.0	306	4	US-09-147-935A-15	Sequence 15, Appl
33	15.8	79.0	306	4	US-09-147-935A-17	Sequence 17, Appl
34	15.8	79.0	306	4	US-09-147-935A-18	Sequence 18, Appl
35	15.8	79.0	306	4	US-09-147-935A-19	Sequence 19, Appl
36	15.8	79.0	306	4	US-09-147-935A-21	Sequence 21, Appl
37	15.8	79.0	306	4	US-09-147-935A-24	Sequence 24, Appl
38	15.8	79.0	306	4	US-09-147-935A-26	Sequence 26, Appl
39	15.8	79.0	306	4	US-09-147-935A-29	Sequence 29, Appl
40	15.8	79.0	306	4	US-09-147-935A-30	Sequence 30, Appl
41	15.8	79.0	306	4	US-09-147-935A-32	Sequence 32, Appl
42	15.8	79.0	306	4	US-09-147-935A-34	Sequence 34, Appl
43	15.8	79.0	306	4	US-09-147-935A-35	Sequence 35, Appl
44	15.8	79.0	306	4	US-09-147-935A-36	Sequence 36, Appl
45	15.8	79.0	306	4	US-09-147-935A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1

US-08-750-088A-70

; Sequence 70, Application US/08750088A

; Patent No. 6329138

; GENERAL INFORMATION:

; APPLICANT: DE BEENHOUWER, HANS

; APPLICANT: PORTAELS, FRAN OISE

; APPLICANT: MACHTELINCX, LIEVE

; APPLICANT: JANNES, GEERT

; APPLICANT: ROSSAU, RUDI

; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC

; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES

; NUMBER OF SEQUENCES: 71

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: US

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/750.088A

; FILING DATE: 21-FEB-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: GOLDSTEIN, JORGE A.

; REGISTRATION NUMBER: 29,021

; REFERENCE/DOCKET NUMBER: 1657.0010000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-750-088A-70

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

Qy 1 tacggtcggcgagctgacc 20
|||||
Db 1 TACGGTCGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tacggtcggcgagctgacc 20
|||||
Db 5 tacggtcggcgagctgacc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tacggtcggcgagctgacc 20
|||||
Db 5 tacggtcggcgagctgacc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tacggtcggcgagctgacc 20
|||||
Db 5 tacggtcggcgagctgacc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

Qy 1 tacggtcggcgagctgacc 20
|||||
Db 5 tacggtcggcgagctgacc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 50
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 tacggtcgccgagctgatcc 20
|||||

Db 5 tacggtcgccgagctgatcc 24
|||||

RESULT 7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313.185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgccgagctgatcc 20

Db 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313.185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgccgagctgatcc 20
|||||

Db 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; Resistance to Rifampin in Mycobacterial Cultures and in

;; TITLE OF INVENTION: Clinical Specimens
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/250,030
;; FILING DATE: 26-MAY-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mueting, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 150.105US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggctggcgagctgatcc 20
|||||

Db 261 TACGGTCGGCGAGCTGATCC 280
|||||

RESULT 10
PCT-US95-06790-1
;; Sequence 1, Application PC/TUS9506790
;; GENERAL INFORMATION:
;; APPLICANT: Mayo Foundation for Medical Education and Research
;; APPLICANT: and Hoffmann-La Roche Inc.
;; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
;; TITLE OF INVENTION: Resistance to Rifampin
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06790
;; FILING DATE: 26-MAY-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Raasch, Kevin W.
;; REGISTRATION NUMBER: 35,651
;; REFERENCE/DOCKET NUMBER: 150.105WO1

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggctggcgagctgatcc 20
|||||

Db 261 TACGGTCGGCGAGCTGATCC 280
|||||

RESULT 11
US-09-147-935A-44
;; Sequence 44, Application US/09147935A
;; Patent No. 6242584
;; GENERAL INFORMATION:
;; APPLICANT: KOOK, Yoon-Hoh
;; APPLICANT: KIM, Bum-Joon
;; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
;; FILE REFERENCE: 0136/0F425
;; CURRENT APPLICATION NUMBER: US/09/147,935A
;; CURRENT FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: PCT/KR98/00228
;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 44
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggtcggcgagctgatcc 20
|||||

Db 6 acggtcggcgagctgatcc 24
|||||

RESULT 12
US-08-750-088A-30
;; Sequence 30, Application US/08750088A
;; Patent No. 6329138
;; GENERAL INFORMATION:
;; APPLICANT: DE BEENHOUWER, HANS
;; APPLICANT: PORTAELS, FRAN OISE
;; APPLICANT: MACHTELINGX, LIEVE
;; APPLICANT: JANNES, GEERT
;; APPLICANT: ROSSAU, RUDI
;; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
;; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: US

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:52:14 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctcggcgagctgatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	US-08-750-088A-70
2	20	100.0	306	4	US-09-147-935A-2
3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-230-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18	90.0	25	4	US-08-750-088A-30
13	16	80.0	306	4	US-09-147-935A-9
14	16	80.0	306	4	US-09-147-935A-10
15	16	80.0	306	4	US-09-147-935A-13
16	16	80.0	306	4	US-09-147-935A-23
17	16	80.0	306	4	US-09-147-935A-31
18	16	80.0	306	4	US-09-147-935A-39
19	16	80.0	306	4	US-09-147-935A-45
20	16	80.0	306	4	US-09-103-840A-2
21	15	75.0	4403765	4	US-09-103-840A-1
22	15	75.0	4411529	4	US-09-103-840A-1
23	14	70.0	50	1	US-08-672-158A-10
24	14	70.0	306	4	US-09-147-935A-10
25	14	70.0	490	1	US-08-133-711-43
26	14	70.0	490	1	US-08-133-711-43
27	14	70.0	6822	4	US-09-426-998-3

c

c	28	14	70.0	7741	4	US-09-426-998-4	Sequence 4, Appl
	29	13	65.0	279	1	US-07-612-674-11	Sequence 11, Appl
	30	13	65.0	306	4	US-09-147-935A-12	Sequence 12, Appl
	31	13	65.0	306	4	US-09-147-935A-14	Sequence 14, Appl
	32	13	65.0	306	4	US-09-147-935A-15	Sequence 15, Appl
	33	13	65.0	306	4	US-09-147-935A-16	Sequence 16, Appl
	34	13	65.0	306	4	US-09-147-935A-18	Sequence 18, Appl
	35	13	65.0	306	4	US-09-147-935A-47	Sequence 47, Appl
	36	13	65.0	408	4	US-09-199-637A-222	Sequence 222, Appl
	37	13	65.0	663	1	US-08-506-404D-1	Sequence 1, Appl
	38	13	65.0	663	3	US-09-035-754-1	Sequence 1, Appl
	39	13	65.0	720	3	US-09-094-359-3	Sequence 3, Appl
	40	13	65.0	720	3	US-09-094-359-5	Sequence 5, Appl
	41	13	65.0	720	3	US-09-094-359-7	Sequence 7, Appl
	42	13	65.0	720	3	US-09-094-359-9	Sequence 9, Appl
	43	13	65.0	720	3	US-09-172-063-11	Sequence 11, Appl
	44	13	65.0	720	3	US-09-172-063-12	Sequence 12, Appl
	45	13	65.0	720	3	US-09-172-063-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6329458
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750.088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-70

Query Match 100.0% Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 1 TACGTCGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 50
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgagctgattcc 20
Db 5 tacggtcgagctgattcc 24

RESULT 7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgagctgattcc 20

Db 18 TACGGTCGGAGCTGATCC 37
RESULT 8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgagctgattcc 20
Db 18 TACGGTCGGAGCTGATCC 37

RESULT 9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in

;; TITLE OF INVENTION: Clinical Specimens
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/250,030
;; FILING DATE: 26-MAY-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mueiting, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 150.105US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
;; Sequence 1, Application PC/TUS9506790
;; GENERAL INFORMATION:
;; APPLICANT: Mayo Foundation for Medical Education and Research
;; APPLICANT: and Hoffmann-La Roche Inc.
;; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
;; TITLE OF INVENTION: Resistance to Rifampin
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06790
;; FILING DATE: 26-MAY-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Raasch, Kevin W.
;; REGISTRATION NUMBER: 35,651
;; REFERENCE/DOCKET NUMBER: 150.105W01

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
;; Sequence 44, Application US/09147935A
;; Patent No. 6242584
;; GENERAL INFORMATION:
;; APPLICANT: KOOK, Yoon-Hoh
;; APPLICANT: KIM, Bum-Joon
;; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;; FILE REFERENCE: 0136/0F425
;; CURRENT APPLICATION NUMBER: US/09/147,935A
;; CURRENT FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: PCT/KR98/00228
;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 44
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 acggtcgcgcgagctgatcc 20
|||||
Db 6 acggtcgcgcgagctgatcc 24

RESULT 12
US-08-750-088A-30
;; Sequence 30, Application US/08750088A
;; Patent No. 6329138
;; GENERAL INFORMATION:
;; APPLICANT: DE BEENHOUWER, HANS
;; APPLICANT: PORTAELS, FRAN OISE
;; APPLICANT: MACHTELINCKX, LIEVE
;; APPLICANT: JANNES, GEERT
;; APPLICANT: ROSSAU, RUDI
;; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
;; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: US

TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgccgagctgatcc 20
|||||
Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
Sequence 1, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105W01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgccgagctgatcc 20
|||||
Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
Sequence 44, Application US/09147935A
Patent No. 6242584
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
APPLICANT: KIM, Yoon-Hoh
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 44
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggtcgccgagctgatcc 20
|||||
Db 6 acggtcgccgagctgatcc 24

RESULT 12
US-08-750-088A-30
Sequence 30, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US

;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 50
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20
|||||
DB 5 tacggctcggcgagctgatcc 24

RESULT 7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20

|||||
DB 18 TACGGTCGGCGAGCTGATCC 37
RESULT 8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20
|||||
DB 18 TACGGTCGGCGAGCTGATCC 37

RESULT 9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; Resistance to Rifampin in Mycobacterial Cultures and

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:48 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20

Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	US-08-750-088A-70
2	20	100.0	306	4	US-09-147-935A-2
3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-250-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18	90.0	25	4	US-08-750-088A-30
13	16	80.0	306	4	US-09-147-935A-4
14	16	80.0	306	4	US-09-147-935A-9
15	16	80.0	306	4	US-09-147-935A-10
16	16	80.0	306	4	US-09-147-935A-13
17	16	80.0	306	4	US-09-147-935A-20
18	16	80.0	306	4	US-09-147-935A-23
19	16	80.0	306	4	US-09-147-935A-31
20	16	80.0	306	4	US-09-147-935A-39
21	16	80.0	306	4	US-09-147-935A-45
22	15	75.0	4403765	4	US-09-103-840A-2
23	15	75.0	4411529	4	US-09-103-840A-1
24	14	70.0	50	1	US-08-672-158A-10
25	14	70.0	306	4	US-09-147-935A-1
26	14	70.0	490	1	US-08-133-711-43
27	14	70.0	6822	4	US-09-426-998-3

c

c	28	14	70.0	7741	4	US-09-426-998-4	Sequence 4, Appl
	29	13	65.0	279	1	US-07-612-674-11	Sequence 11, Appl
	30	13	65.0	306	4	US-09-147-935A-12	Sequence 12, Appl
	31	13	65.0	306	4	US-09-147-935A-14	Sequence 14, Appl
	32	13	65.0	306	4	US-09-147-935A-15	Sequence 15, Appl
	33	13	65.0	306	4	US-09-147-935A-16	Sequence 16, Appl
	34	13	65.0	306	4	US-09-147-935A-18	Sequence 18, Appl
	35	13	65.0	306	4	US-09-147-935A-47	Sequence 47, Appl
	36	13	65.0	408	4	US-09-199-637A-222	Sequence 222, App
	37	13	65.0	663	1	US-08-506-404D-1	Sequence 1, Appl
	38	13	65.0	663	3	US-09-035-754-1	Sequence 1, Appl
	39	13	65.0	720	3	US-09-094-359-3	Sequence 3, Appl
	40	13	65.0	720	3	US-09-094-359-5	Sequence 5, Appl
	41	13	65.0	720	3	US-09-094-359-7	Sequence 7, Appl
	42	13	65.0	720	3	US-09-094-359-9	Sequence 9, Appl
	43	13	65.0	720	3	US-09-172-063-11	Sequence 11, Appl
	44	13	65.0	720	3	US-09-172-063-12	Sequence 12, Appl
	45	13	65.0	720	3	US-09-172-063-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
Sequence 70, Application US/08750088A
Patent No. 6929033
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-750-088A-70

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 1 TACGGTCGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657-0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-750-088A-30

Query Match 90.0%; Score 18; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 cggtcgagcgtgatcc 20
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 CGTGGCGAGCTGATCC 25

RESULT 13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium aurum
US-09-147-935A-4

Query Match 80.0%; Score 16; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gtcgagcgtgatcc 20
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 gtcgagcgtgatcc 24

RESULT 14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:

; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 9
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9

Query Match 80.0%; Score 16; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gtcgagcgtgatcc 20
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 gtcgagcgtgatcc 24

RESULT 15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 10
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10

Query Match 80.0%; Score 16; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gtcgagcgtgatcc 20
| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 gtcgagcgtgatcc 24

Search completed: August 7, 2002, 23:51:52
Job time: 7178 sec

Thu Aug 8 09:35:15 2002

us-09-786-105-3.oli.rni

Page 6

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:26 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctgcgcgcgcgcgcgcgc 20

Scoring table: **OLIGO_NUC**
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_jnu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006564	AE006564 Mycobacte
18	20	100.0	19770	1	MTC1376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18	90.0	25	6	A47816	A47816 Sequence 30
22	18	90.0	87	6	AX050338	AX050338 Sequence
23	17	85.0	17407	1	AE006976	AE006976 Mycobacte
24	17	85.0	68848	1	MTV043	AL022004 Mycobacte
25	16	80.0	306	1	AF057456	AF057456 Mycobacte
26	16	80.0	306	1	AF057459	AF057459 Mycobacte
27	16	80.0	306	1	AF057460	AF057460 Mycobacte
28	16	80.0	306	1	AF057463	AF057463 Mycobacte
29	16	80.0	306	1	AF057471	AF057471 Mycobacte
30	16	80.0	306	1	AF057473	AF057473 Mycobacte
31	16	80.0	306	1	AF057480	AF057480 Mycobacte
32	16	80.0	306	1	AF057489	AF057489 Mycobacte
33	16	80.0	306	1	AF057496	AF057496 Corynebac
34	16	80.0	306	1	AE173087	AE173087 Mycobacte
35	16	80.0	306	6	AR157005	AR157005 Sequence
36	16	80.0	306	6	AR157010	AR157010 Sequence
37	16	80.0	306	6	AR157011	AR157011 Sequence
38	16	80.0	306	6	AR157014	AR157014 Sequence
39	16	80.0	306	6	AR157021	AR157021 Sequence
40	16	80.0	306	6	AR157024	AR157024 Sequence
41	16	80.0	306	6	AR157032	AR157032 Sequence
42	16	80.0	306	6	AR157040	AR157040 Sequence
43	16	80.0	306	6	AR157046	AR157046 Sequence
44	16	80.0	2440	1	SIGROSEL	X95970 S. lividans
45	16	80.0	3000	1	SCGROEL	X75206 S. coelicolo

ALIGNMENTS

RESULT	1
AF057450	306 bp DNA linear BCT 17-SEP-1999
LOCUS	Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
DEFINITION	
ACCESSION	AF057450
VERSION	AF057450.1 GI:5902487
KEYWORDS	
SOURCE	
ORGANISM	Mycobacterium africanum.
REFERENCE	Mycobacterium africanum
AUTHORS	Bacteria: Firmicutes: Actinobacteria: Actinobacteridae: Actinomycetales: Corynebacterineae: Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex.
TITLE	1 (bases 1 to 306)
JOURNAL	Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
MEDLINE	Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
POBMD	J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
REFERENCE	2 (bases 1 to 306)
AUTHORS	Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gong-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

source

Location/Qualifiers

1. .306
/organism="Mycobacterium africanum"
/strain="ATCC25420"
/db_xref="ATCC:25420"
/db_xref="taxon:33894"
<1. .>306
/gene="rpoB"
/gene="rpoB"
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta"
/protein_id="A055514.1"
/db_xref="GI:5902488"
/translation="RTVGELIQNIRVGSRMERYRERMTPDVEATPOTLINIRP
VVAIKKEFFGTSQLSOFMDONNPLSGLTJHKKRLSALPGSLRRAGLEVRDHPSH"

gene

CDS

BASE COUNT

56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgagcgtgacc 20
|||||
Db 5 TACGCTCGGCGAGCTGATCC 24

RESULT 2

AF057451

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 4

LOCUS AF057453 306 bp DNA linear BCT 17-SEP-1999

DEFINITION Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057453

VERSION AF057453.1 GI:5902493

KEYWORDS

SOURCE Mycobacterium bovis BCG.

ORGANISM Mycobacterium bovis BCG.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J Clin. Microbiol. 37 (6), 1714-1720 (1999)

TITLE J Clin. Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756

MEDLINE 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H.,
Kim,S.-J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

source 1..306
/organism="Mycobacterium bovis BCG"
/strain="Tokyo 1172"
/db_xref="taxon:33892"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta"
/protein_id="AAD5517.1"
/db_xref="GI:5902494"
/translation="RTVGELIQNIRVGSRMERYRREMTTQDEAITPOTLINIRP
VVAATKEFGTSQISQFMDONNPISGLTHKRRLSALGPGGLSREKAGLEVDRVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcagctgaccc 20
|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 5

LOCUS AF057454 306 bp DNA linear BCT 08-OCT-1999

DEFINITION Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057454

VERSION AF057454.1 GI:5902495

KEYWORDS

SOURCE Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J Clin. Microbiol. 37 (6), 1714-1720 (1999)

TITLE J Clin. Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756

MEDLINE 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H.,
Kim,S.-J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

source 1..306
/organism="Mycobacterium tuberculosis"
/strain="H37Rv; ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:1773"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta"
/protein_id="AAD5518.1"
/db_xref="GI:5902496"
/translation="RTVGELIQNIRVGSRMERYRREMTTQDEAITPOTLINIRP
VVAATKEFGTSQISQFMDONNPISGLTHKRRLSALGPGGLSREKAGLEVDRVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcagctgaccc 20
|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 6

LOCUS AR157003 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 2 from patent US 6242584.

ACCESSION AR157003

VERSION AR157003.1 GI:15125707

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 306)
Kook,Y. and Kim,B.
Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
Patent: US 6242584-A 2 05-JUN-2001;

TITLE Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene

JOURNAL Patent: US 6242584-A 2 05-JUN-2001;

FEATURES

source 1..306
/organism="unknown"
/strain="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcagctgaccc 20
|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y.-H. and Kim,B.-J.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 8
LOCUS ARI57008 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 9
LOCUS ARI57042 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 10
LOCUS ARI57051 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37)
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Mycobacterium; Mycobacteriaceae; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

FEATURES

Location/Qualifiers
 1..432
 /organism="Mycobacterium tuberculosis"
 /strain="H37"
 /db_xref="taxon:1773"
 CDS
 <1..>432
 /codon_start=1
 /transl_table=1
 /product="RNA polymerase beta subunit"
 /protein_id="AAB58068.1"
 /db_xref="GI:149992"
 /translation="GNRLRTVGLIQNIVGHSRMERYRRTTODVEAITPOTL
 INRPVVAIKEFTQSOFMDONNLSGLTHKRLSALGPGGLSRRAGLEVRDV
 HPSHYGRMCPIETPEGNIGLISLYAVRVNPGFIETPYR"
 149
 /phenotype="rifampicin resistant in association with
 mutation 234 G"
 /replace="C"
 188
 /phenotype="rifampicin resistant"
 /replace="C"
 191
 /phenotype="rifampicin resistant in association with
 mutation 203 T"
 /replace="C"
 194
 /phenotype="rifampicin resistant"
 /replace="T"
 203
 /phenotype="rifampicin resistant"
 /replace="T"
 208..210
 /phenotype="rifampicin resistant"
 /replace=""
 232
 /phenotype="rifampicin resistant"
 /replace="G"
 232
 /phenotype="rifampicin resistant"
 /replace="G"
 233
 /phenotype="rifampicin resistant"
 /replace="a"
 233
 /phenotype="rifampicin resistant"
 /replace="g"
 233
 /phenotype="rifampicin resistant"
 /replace="c"
 234
 /phenotype="rifampicin resistant"
 /replace="g"
 247..248
 /phenotype="rifampicin resistant"
 /replace="ca"
 248
 /phenotype="rifampicin resistant"
 /replace="g"
 248
 /phenotype="rifampicin resistant"
 /replace="t"
 254
 /phenotype="rifampicin resistant"
 /replace="C"
 140 C 148 g 67 t

BASE COUNT

77 a 140 c 148 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgactgacc 20

DB 18 TACGTCGCGCAGCTGATCC 37

RESULT 12

AR067448

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

432 bp

DNA

linear

PAT 29-SEP-1999

Sequence 59 from patent US 5851763.

AR067448

GI:5998670

Unknown.

Unclassified.

1 (bases 1 to 432)

Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and

Bodmer,T.

Rapid detection of antibiotic resistance in mycobacterium

tuberculosis

Patent: US 5851763-A 59 22-DEC-1998;

Location/Qualifiers

1..432

/organism="unknown"

77 a 139 c 149 g 67 t

Query Match

100.0%; Score 20; DB 6; Length 432;

Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgactgacc 20

DB 18 TACGTCGCGCAGCTGATCC 37

RESULT 13

150706

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..970

/organism="unknown"

BASE COUNT

ORIGIN

970 bp

DNA

linear

PAT 07-OCT-1997

Sequence 1 from patent US 5643723.

150706

GI:2472409

Unknown.

Unclassified.

1 (bases 1 to 970)

Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.

and Whelan,A.Christian.

Detection of a genetic locus encoding resistance to rifampin in

mycobacterial cultures and in clinical specimens

Patent: US 5643723-A 1 01-JUL-1997;

Location/Qualifiers

1..970

/organism="unknown"

182 a 302 c 330 g 156 t

Query Match

100.0%; Score 20; DB 6; Length 970;

Best Local Similarity 100.0%; Pred. No. 3.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgactgacc 20

DB 261 TACGTCGCGCAGCTGATCC 280

RESULT 14

AX111339

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

3534 bp

DNA

linear

PAT 30-APR-2001

Sequence 2072 from Patent WO0123604.

AX111339

GI:13927631

Unknown.

Unclassified.

1 (bases 1 to 3534)

Myers,D., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and

Bodmer,T.

Rapid detection of antibiotic resistance in mycobacterium

tuberculosis

Patent: US 5851763-A 59 22-DEC-1998;

Location/Qualifiers

1..3534

/organism="unknown"

182 a 302 c 330 g 156 t

Myobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3853)
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
FEATURES Infectio Diagnostic (I.D.I.) INC. (CA)
source Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggtcgcgcagctgaccc 20
|||||
Db 1137 TACGCTCGCGAGCTGATCC 1156
RESULT 15
LOCUS MTU12205 3853 bp DNA linear BCT 02-MAR-2000
DEFINITION Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3853)
AUTHORS Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
Cole,S., Schopfer,K. and Burkart,T.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3853)
AUTHORS Imboden,P.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
FEATURES Location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
576..>3853
/gene="rpoB"
/codon_start=1
/transl_table=1
/product="RNA-polymerase beta subunit"
/protein_id="AA02042.2"
/db_xref="GI:714499"
/translation="MLEGCIADSRGSKTAASPSRSSNNNSVGPANRYFAKL
REPLEVGLDVOTDSFEMILIGSPRMRESAERGDVNPVCGLEBYELKSLPIEDFSSG
MSLSFSDPRPDYKAVDECDKDKMTYAAPLVTAERINNNGEIKSQTVFMGDFPDM
TEKGTFLINGTERVVSQIVRSRGVYDFDETIDKSTDKTLHSKVIVPSRGAMLEFDYDK
RDYVGRIDRRKQRPVTLKALGWTSEQIVERSSEIKMRSTLEKNDYVGTDEALD
IYRKLREPPEPTKESQTLLENLEFFEKERYDLARVGRYKYNKKLGLHVGEPITSSLT

EDVYATTEIVLHEGOTTTPVPGVVEYEDDDIHFGNRLRTVIGELLIONIRVG
MSRREVRREKMTQDVVETPTPLINIRPVAAIKFEFTSQISQMDNNPLSGLT
HKRLSLAPGSLRERAGLEVDRVHPSHYGRMCPIETPGPNIGLSLSYARAP
FGELETYRKVVDGVSDGIYLTADESDRHVAOANSPIDADGRFVYRVRKAG
EVEYPSSEVDYMDVSPROMYSVATAMIPLEHDDARALMGAMORQAVPIVRSEAP
LVGTMELRAAIDAATSSOSGVIIEVSADYITVMHNDTRTRYRKRARSNHGC
ANOCPIYDADRVYAGVITADGECTDGEALGNLVAIMPEGHNTEDATILSNL
VEEDVLSIHIEHEIDARDTKLGAEEITTDIPNISDEVLADDERGIVRIGAEVRG
DILGKVTPEGETELTPEERLRAIFEGKAREVDTSLKVPHGSKVIGIRVFSRED
EDELPAVNMELVRYVYQKRKISDGDKLAGRHNKGVIGKILPVEDMPLADGTPVDI
ILNTHGVPRRMNIGQILETHLGMCAHSGMKVDAKGVDMNAARLPDELLPAOPNAIVS
TPVFDGAOEALDGLSCTLPNRGDVLYVADKAMLPDGRSGEPPEPYTVVYMYM
KLHLVYDKIHARSTGYSMTIQPPLGSKAQFGQRGKEHCNMAQVGAATYLOELL
TIKS"
BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. NO. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggtcgcgcagctgaccc 20
|||||
Db 1712 TACGCTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 23:49:01
Job time: 9215 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 20:08:01 : Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 taacgctgcgcagcgtatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapect 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estcu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estt2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	422	10	BE443802 WHE1122_B
2	17	85.0	544	10	BE445100 WHE1132_H
3	17	85.0	538	10	BE444713 WHE1137_H
4	17	85.0	610	9	BE195103 BE195103 HVSMEH008
5	17	85.0	658	10	BE442518 WHE1101_H
6	17	85.0	828	10	BG299722 HVSME002
7	16	80.0	130	10	BM397871 5009-0-38
8	16	80.0	132	10	BM396091 5009-0-17
9	16	80.0	134	10	BM396255 5009-0-42
10	16	80.0	606	10	BI981973 BI981973 fu3f08.y
11	16	80.0	640	10	BI888442 2F637-2-0
12	16	80.0	708	10	BE585978 Est#7PT7
13	15	75.0	237	10	BE423869 WHE0067_F
14	15	75.0	376	9	AT945868 bs17g07.y
15	15	75.0	379	9	AT944952 bs07c12.y
16	15	75.0	556	12	BH229591 1006153C0
17	15	75.0	568	10	BI628597 RH57079.5

18	15	75.0	652	10	BE489438
19	15	75.0	655	10	BE489430
20	15	75.0	667	10	BE489536
21	15	75.0	703	10	BE496035
22	15	75.0	722	10	BE496005
23	15	75.0	958	10	BE969326
24	15	75.0	984	12	CNS01G72
25	15	75.0	1000	10	BG416363
26	15	75.0	1188	10	BM477266
27	14	70.0	159	10	BI727507
28	14	70.0	180	10	C61884
29	14	70.0	239	10	BF920601
30	14	70.0	251	12	A0906217
31	14	70.0	252	10	W87730
32	14	70.0	292	9	BB347857
33	14	70.0	299	10	BI133481
34	14	70.0	318	10	M79472
35	14	70.0	328	9	AW922029
36	14	70.0	329	10	H57342
37	14	70.0	339	9	AJ781216
38	14	70.0	344	10	BE415176
39	14	70.0	349	9	AU110574
40	14	70.0	349	10	BG274757
41	14	70.0	352	10	T83696
42	14	70.0	360	9	AV186178
43	14	70.0	360	9	AV191317
44	14	70.0	360	9	AV192208
45	14	70.0	360	9	AV197881

ALIGNMENTS

RESULT 1
BE443802 422 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1122.B06.C12Zs Wheat etiolated seedling root normalized CDNA
DEFINITION library Triticum aestivum CDNA clone WHE1122_B06.C12, mRNA
sequence.
ACCESSION BE443802
VERSION BE443802.1 GI:9443341
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
1 (bases 1 to 422)
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.D., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Scratagene SK primer.
Location/Qualifiers
1..422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122_B06.C12"
/clone_lib="Wheat etiolated seedling root normalized CDNA
library"
/tissue_type="Root"

FEATURES

source

```

/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give plasmid phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

BASE COUNT 84 a 130 c 124 g 84 t

ORIGIN

```

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 4 ggtcggcagctgattcc 20
    |||||||
Db 86 ggtcggcagctgattcc 102
```

```

RESULT 2
BE445100 544 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_H08_P16Z5 Wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
sequence.
ACCESSION BE445100
VERSION BE445100.1 GI:9444655
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 544)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..544
```

```

FEATURES
Source
1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
```

```

/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give plasmid phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

BASE COUNT 121 a 173 c 132 g 118 t

ORIGIN

```

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 4 ggtcggcagctgattcc 20
    |||||||
Db 512 ggtcggcagctgattcc 528
```

```

RESULT 3
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1137_H03_005Z5 Wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713
VERSION BE444713.1 GI:9444264
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 558)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..558
```

```

FEATURES
source
1..558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
```

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the *λ* Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give plasmid phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcgcgagcgtcatcc 20
|||||
Db 514 GGTGCGGAGCTGATCC 530

RESULT 4
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEH0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCEDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0088E21f,
mRNA sequence.

ACCESSION BE195103 GI:16321083
VERSION BE195103.3
KEYWORDS
SOURCE
ORGANISM

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bp bases = 238
Seq primer: AATTACCCCTCAGTAAGCG
High quality sequence stop: 563.
Location/Qualifiers

FEATURES
source
1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0088E21f"
/clone.lib="Hordeum vulgare 5-45 DAP spike EST library
HVCEDNA0009 (5 to 45 DAP)"
/tissue.type="5-45 DAP spike"
/lab.host="SOLR"
/note="Vector: lambdaZAP. Site.1: EcoRI, Site.2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,

30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million plv were in vivo excised to give plasmid phagemids (Choi) in the *λ* Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phed valve 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30 (<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT 127 a 203 c 158 g 120 t
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcgcgagcgtcatcc 20
|||||
Db 499 GGTGCGGAGCTGATCC 515

RESULT 5
LOCUS BE442518 658 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1101_H10_O19Zs Wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA
sequence.

ACCESSION BE442518 GI:9442034
VERSION BE442518.1
KEYWORDS
SOURCE
ORGANISM

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 658)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers

FEATURES
source
1..658
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
/clone.lib="Wheat etiolated seedling root normalized cDNA
library"

```

/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid
pluscript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Clonase lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pluscript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT      144 a      209 c      105 g      140 t
ORIGIN
Query Match      85.0%; Score 17; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4      ggtcgagcgagctgaccc 20
          ||||||||||||||||
Db      512      ggtcgagcgagctgaccc 528

RESULT 6
LOCUS      BG299722      828 bp      mRNA      linear      EST 17-OCT-2001
DEFINITION      HVSMEa0021120f Hordeum vulgare seedling shoot EST library
                  HVCNDA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
                  mRNA sequence.
ACCESSION      BG299722
VERSION      BG299722.1 GI:13087434
KEYWORDS      EST.
SOURCE      Hordeum vulgare
ORGANISM      Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 828)
Wing,R., Close,T.J., Kleinhof,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.,
Fenton,R.D. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex cold-stressed seedling shoot cDNA
library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 574
Seq primer: AATTAAACCTCAGTAAGGG
High quality sequence stop: 643.
Location/Qualifiers
1..828
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEa0021120f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCNDA0001 (Cold stress)"
/tissue_type="Seedling shoot"

```

```

/lab_host="TJc121"
/notes="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 50c for 2 days. Shoots were then harvested,
total RNA was prepared. poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 600000 plu
were in vivo excised to give pluscript SK(-) cDNA
phagemids. These steps were performed in the TJ Close
Laboratory at the University of California, Riverside
(Choi, Close, Fenton). Phagemids were plated and picked at
the Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
, DNA sequencing and sequence analysis were performed at
CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhof A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      172 a      271 c      220 g      165 t
ORIGIN
Query Match      85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4      ggtcgagcgagctgaccc 20
          ||||||||||||||||
Db      500      ggtcgagcgagctgaccc 516

RESULT 7
LOCUS      BM397871/c      130 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
                  Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM397871
VERSION      BM397871.1 GI:18197924
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila.
ORGANISM      Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomata; Tetrahymenina; Tetrahymena.
1 (bases 1 to 130)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kik,K.E., Frankel
,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)

```


BASE COUNT 26 a 41 c 44 g 18 t 1 others
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 130;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 gtcggcagcgtatcc 20
|||||
Db 90 GTCGGCAGCTGATCC 75

RESULT 8
BM396091/c 132 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-17-B01.t.1 Chllocoat/Turkewiltz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM396091
VERSION BM396091.1 GI:18196144
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 132)
AUTHORS Turkewiltz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewiltz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
Source Location/Qualifiers

1..132
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chllocoat/Turkewiltz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chllocoat and Turkewiltz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 27 a 42 c 44 g 19 t
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 gtcggcagcgtatcc 20
|||||
Db 92 GTCGGCAGCTGATCC 77

RESULT 9
BM398255/c 134 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-42-H08.t.1 Chllocoat/Turkewiltz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398255
VERSION BM398255.1 GI:18196308
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 134)
AUTHORS Turkewiltz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewiltz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
Source Location/Qualifiers

1..134
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chllocoat/Turkewiltz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chllocoat and Turkewiltz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT 26 a 44 c 46 g 18 t
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 gtcggcagcgtatcc 20
|||||
Db 94 GTCGGCAGCTGATCC 79

RESULT 10
BI981973/c 606 bp mRNA linear EST 24-OCT-2001
LOCUS
DEFINITION BI981973.1 zebrafish adult brain Dario rerio cDNA clone 533151 5'
similar to TR:Q9Y4D4 Q9Y4D4 KIA0648 PROTEIN;; mRNA sequence.
BI981973
BI981973.1 GI:16371108
EST.
SOURCE zebrafish.
ORGANISM Dario rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Dario.

REFERENCE 1 (bases 1 to 606)
AUTHORS Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
TITLE Washu zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: fu53f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
CDNA Library Preparation: John Neal, CDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
High quality sequence stop: 446.

FEATURES

source

Location/Qualifiers

1..606
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_lib="zebrafish adult brain"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="E. coli DH10B"
 /note="Vector: pZiPlox; Site_1: NotI; Site_2: SalI.
 Original library was constructed in lambdaZiPlox. Mass
 excision of the cDNA library was performed to yield
 pZiPlox plasmids. Insert check was done in original
 library."
 BASE COUNT 209 a 133 c 139 g 125 t
 ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 606;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcagctg 16
 |||
 Db 452 TACGCTCGCGAGCTG 437

RESULT 11 640 bp mRNA linear EST 12-OCT-2001
 BI888442 ZR637-2-000197 zebrafish shield stage whole embryo cDNA library
 LOCUS MPMGP637.Danio rerio cDNA clone MPMGP637_18E17;MPMGP637E17 5',
 DEFINITION mRNA sequence.
 ACCESSION BI888442
 VERSION BI888442.1 GI:16095713
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.
 1 (bases 1 to 640)
 Clark M., Anstad, P., Hennig, S., Johnson, S.L. and Lehrach, H.
 EST sequencing of a zebrafish shield stage cDNA library normalised
 by oligonucleotide fingerprinting
 JOURNAL Unpublished (2001)
 COMMENT Contact: Hennig S
 Laboratory 123, dept. Lehrach
 Max-Planck-Institut fuer Molekulare Genetik
 Ihnestr.63-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1612
 Fax: +49 30 8413 1380
 Email: hennig@molgen.mpg.de
 5' EST sequencing of clones from a zebrafish shield stage library,
 normalised from 55,000 starting clones by oligonucleotide
 fingerprinting
 High quality sequence stop: 640.
 Location/Qualifiers

FEATURES

Location/Qualifiers

1..640
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_lib="zebrafish shield stage whole embryo cDNA
 library MPMGP637"
 /tissue_type="whole embryo"
 /dev_stage="shield stage, 6 hrs post-fertilisation"
 /lab_host="E. coli, XL1 blue MRF"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
 oligo-dT-NotI primed. SalI adaptors, directionally cloned,
 library normalised by oligonucleotide fingerprinting"
 BASE COUNT 209 a 152 c 139 g 139 t
 ORIGIN

BASE COUNT

209 a 152 c 139 g 139 t
 ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 640;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcagctg 16
 |||
 Db 541 TACGCTCGCGAGCTG 526

RESULT 12 708 bp mRNA linear EST 17-AUG-2000
 BE585978 Est#7PT7_A09.a9_065 KSU wheat Fusarium graminearum infected spike
 LOCUS cDNA library Trilicium aestivum cDNA clone Est#7PT7_A09.a9_065, mRNA
 DEFINITION sequence.
 ACCESSION BE585978
 VERSION BE585978.1 GI:9839010
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Trilicium aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triliceae; Trilicium.
 1 (bases 1 to 708)
 Fellers, J.P., Li, W.L., Hill-Ambroz, K., Matthews, A. and Gill, B.S.
 The structure and function of the expressed portion of the wheat
 genomes - Kansas State University. Fusarium graminearum infected
 spike cDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Fellers
 US Department of Agriculture, Agriculture Research Service, Plant
 Science and Entomology Unit
 Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
 University, Manhattan, KS 66506, USA
 Tel: 785-532-2367
 Fax: 785-532-6167
 Email: jpf@iaila.ksu.edu
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: T7.
 Location/Qualifiers

FEATURES

Location/Qualifiers

1..708
 /organism="Trilicium aestivum"
 /cultivar="Sumai3"
 /db_xref="taxon:4565"
 /clone_lib="Est#7PT7_A09.a9_065"
 /clone_lib="KSU wheat Fusarium graminearum infected spike
 cDNA library"
 /tissue_type="Spike"
 /dev_stage="Adult plant"
 /lab_host="E. coli JM109"
 /note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
 Plants were grown in the greenhouse. Spikes were sprayed
 with Fusarium graminearum (at what stage). Total RNA, and
 poly(A) RNA were prepared from infected spikes. cDNA was
 prepared using the SmartRTP PCR cDNA synthesis kit from
 Clontech. cDNA was cloned into the pGEM-T easy vector
 from Promega."
 BASE COUNT 154 a 221 c 177 g 156 t
 ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 708;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gtgcgcagctgctcc 20
 |||
 Db 559 GTGCGCGAGCTGATCC 574

RESULT 13
BE423869/c
LOCUS
DEFINITION WHE0067_F05_K092S wheat endosperm cDNA library Triticum aestivum
ACCESSION BE423869
VERSION WHE0067_F05_K09, mRNA sequence.
KEYWORDS
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 237)
Altenbach, S., Anderson, O.D., Chao, S., Galli, G., Han, P.S., Hsia
C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and
Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Endosperm cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..237
/organism="Triticum aestivum"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0067_F05_K09"
/clone_1lb="Wheat endosperm cDNA library"
/tissue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
EcoRI; Seeds collected, endosperm isolated, and RNA
prepared by Susan Altenbach. Library constructed by
Stratagene, Inc. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab."

BASE COUNT 65 a 79 c 40 g 53 t
ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 tcgagcgagctgaccc 20
|||||
Db 79 TCGCGAGCTGATCC 65

RESULT 14
AI945868
LOCUS
DEFINITION bs17607.y1 Drosophila melanogaster adult testis library Drosophila
ACCESSION AI945868
VERSION bs17607 5', mRNA sequence.
KEYWORDS
SOURCE EST.
ORGANISM Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 376)
Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and

TITLE Oliver, B.
JOURNAL Gene discovery using computational and microarray analysis of
MEDLINE transcription in the drosophila melanogaster testis
20568492
On Aug 17, 1999 this sequence version replaced gi:5736266.
COMMENT
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@helix.nih.gov,
http://www.nidk.nih.gov/intram/people/boliver.htm
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.nidk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 17 row: 9 column: 07
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..376
/organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bs17607"
/clone_1lb="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis. Vector: pBluescript SK (Stratagene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/y males raised at 25°C. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA synthesis
kit. Oligo dt-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

BASE COUNT 110 a 94 c 107 g 65 t
ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 acggtcggagcgctg 16
|||||
Db 272 ACGGTGCGCGAGCTG 286

RESULT 15
AI944952
LOCUS
DEFINITION bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
ACCESSION AI944952
VERSION bs07c12 5', mRNA sequence.
KEYWORDS
SOURCE EST.
ORGANISM Drosophila melanogaster
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 379)
Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and
Oliver, B.
Gene discovery using computational and microarray analysis of
transcription in the drosophila melanogaster testis

JOURNAL
MEDLINE
COMMENT

Genome Res. 10 (12), 2030-2043 (2000)
20568492

On Aug 17, 1999 this sequence version replaced gi:5735350.

Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239

Email: oliverbhelix.nih.gov,
<http://www.nidddk.nih.gov/intram/people/boliver.htm>
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
<http://www.nidddk.nih.gov/intram/people/boliver.htm>). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
Plate: 07 row: c column: 12

Seq primer: M13RPL reverse primer (ABI).

FEATURES
Source

1. 379
Location/Qualifiers
/organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bs07c12"
/clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBluescript SK (Stratagene);
Site 1: EcoR I; Site 2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/y males raised at 25°C. RNA
isolated using RNeasy (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA synthesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

BASE COUNT 104 a 96 c 113 g 66 t
ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 acggtcgagcagctg 16
|||||
Db 39 ACGGTGGCGGAGCTG 53

Search completed: August 7, 2002, 23:12:30
Job time: 11069 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:30 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 taagcgcttcgatgacc 20

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:
1: em_estdb:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_hic:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	234	10	W06754 SMEST0390 S
2	17	85.0	579	10	T24127
3	16	80.0	624	10	BE896357
4	15	75.0	384	10	BM077908
5	15	75.0	452	9	AM694629
6	15	75.0	517	12	TA247H04P
7	15	75.0	536	12	A0783856
8	15	75.0	537	12	TA140G03P
9	15	75.0	540	12	TA190A10P
10	15	75.0	631	12	BH615799
11	15	75.0	690	9	BE053145
12	15	75.0	1033	12	CNSD40XP
13	15	75.0	1218	10	BM007170
14	14	70.0	247	9	AV640031
15	14	70.0	269	9	AV640876
16	14	70.0	288	9	BB177553
17	14	70.0	336	12	A0660540

C	18	14	70.0	390	9	AV644609	AV644609
C	19	14	70.0	416	9	AJ284239	AJ284239
C	20	14	70.0	421	12	A2813806	A2813806
C	21	14	70.0	428	10	BK252718	BK252718
C	22	14	70.0	431	9	AW280184	AW280184
C	23	14	70.0	466	9	AF051116	AF051116
C	24	14	70.0	472	10	BE449520	BE449520
C	25	14	70.0	474	9	AV396989	AV396989
C	26	14	70.0	476	9	A1483656	A1483656
C	27	14	70.0	477	9	A1488127	A1488127
C	28	14	70.0	489	9	AM618736	AM618736
C	29	14	70.0	497	9	AV643117	AV643117
C	30	14	70.0	508	9	AV642711	AV642711
C	31	14	70.0	518	9	AV642141	AV642141
C	32	14	70.0	525	9	AM650840	AM650840
C	33	14	70.0	531	9	AV642766	AV642766
C	34	14	70.0	544	12	A0843909	A0843909
C	35	14	70.0	556	9	AM155814	AM155814
C	36	14	70.0	562	12	BH487728	BH487728
C	37	14	70.0	566	9	AV631818	AV631818
C	38	14	70.0	582	12	CNS01K68	CNS01K68
C	39	14	70.0	626	9	AM442770	AM442770
C	40	14	70.0	626	9	BB640393	BB640393
C	41	14	70.0	628	10	BE270176	BE270176
C	42	14	70.0	664	10	BG102752	BG102752
C	43	14	70.0	670	12	A0943645	A0943645
C	44	14	70.0	672	12	A0943372	A0943372
C	45	14	70.0	676	9	A1491107	A1491107

ALIGNMENTS

RESULT 1
W06754/c 234 bp mRNA linear EST 01-JUL-1996
LOCUS SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Franco,G.R. and Pena,S.D.J.
TITLE Strigeidida, Schistosomatidae; Schistosoma.
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Biologia
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES

1..234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lambda) BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells."

BASE COUNT 49 a 84 c 66 g 33 t 2 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaa 17
|||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 2

T24127 579 bp mRNA linear EST 27-FEB-1995
T24127/c SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
T24127
T24127.1 GI:529730

EST.
Schistosoma mansoni.
SOURCE

REFERENCE
AUTHORS Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeldida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 579)
Francisco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.
and Pena, S.D.J.
Identification of new Schistosoma mansoni genes by the EST strategy
using a directional cDNA library
Gene 152, 141-147 (1995)

JOURNAL
MEDLINE Contact: Franco G.R. and Pena S.D.J.
95137379 Laboratório de Genética-Bioquímica, Departamento de Bioquímica
Imunologia
Instituto de Ciências Biológicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.

FEATURES
SOURCE Location/Qualifiers
1. 579

/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_1ib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
Total cellular RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
Guanidine Thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid
DNA (lambda) BA vector, a phagemid derived from pEMBL,
Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and
electroporated into E. coli strain DH10B (BRL). The
library was amplified and further selected for clones
containing long inserts (>500 bp) by purification of the
plasmid DNA from a fragment of a 1% low-melting-point
agarose gel, containing the smear of the library and
electroporation into DH10B cells."

BASE COUNT 102 a 206 c 179 g 88 t 4 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaa 17
|||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 3

BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5',
DEFINITION mRNA sequence.
BE896357
BE896357.1 GI:10360678

EST.
human.
SOURCE

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 624)
NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: ATCC/DC/DMP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers

FEATURES
SOURCE Location/Qualifiers
1. 624

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_1ib="NIH-MGC-72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPOr6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 155 a 209 c 150 g 110 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gcggttcgatgacc 20
|||||
Db 582 GCCTTCGATGACCC 597

RESULT 4
LOCUS BM077908 384 bp mRNA linear EST 14-NOV-2001
DEFINITION p51g06.y1 Ancylostoma caninum L3 SS SL1 TOPO VI Murphy Chiapelli
McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION BM077908
VERSION
KEYWORDS
SOURCE dog hookworm.
ORGANISM Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Strongyliida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 384)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wyle,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,T.,
Gibbons,M., Rittler,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
Ronko,T., Kennedy,S., Maguire,L., Beck,C., Underwood,R., Steptoe,
'M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarter at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center.
Location/Qualifiers
1. 384
/organism="Ancylostoma caninum"
/db_xref="taxon:29170"
/clone_lib="Ancylostoma caninum L3 SS SL1 TOPO VI Murphy
Chiapelli McCarter"
/dev_stage="Serum stimulated L3"
/lab_host="DH10B"
/note="Vector: PCRIT-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
Murphy, Brandi Chiapelli, and Dr. James McCarter at
Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Ancylostoma caninum SS/LS cDNA PCR products of
size >400 nucleotides containing SL1 on the 5' end and
oligo(dT) on the 3' end were non-directionally cloned
into PCRIT-TOPO(Invitrogen) following the TOPO TA cloning
protocol. Nematodes were provided by Dr. Prema Arasu
(Prema.Arasu@ncsu.edu) of North Carolina State University
in Raleigh, NC."

BASE COUNT 116 a 71 c 85 g 112 t
ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgacgaac 18
|||||
DB 324 GCGCTTCGATGAC 338

RESULT 5
LOCUS AM694629/c 452 bp mRNA linear EST 21-DEC-2000
DEFINITION NF078E03ST1021 Developing stem Medicago truncatula cDNA clone
NF078E03ST 5', mRNA sequence.
ACCESSION AM694629
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Strongyliida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 384)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wyle,T.,
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,T.,
Gibbons,M., Rittler,E., Bennett,J., Franklin,C., Tsagarisvilli,R.,
Ronko,T., Kennedy,S., Maguire,L., Beck,C., Underwood,R., Steptoe,
'M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli, and
Dr. James McCarter at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center.
Location/Qualifiers
1. 384
/organism="Ancylostoma caninum"
/db_xref="taxon:29170"
/clone_lib="Ancylostoma caninum L3 SS SL1 TOPO VI Murphy
Chiapelli McCarter"
/dev_stage="Serum stimulated L3"
/lab_host="DH10B"
/note="Vector: PCRIT-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
Murphy, Brandi Chiapelli, and Dr. James McCarter at
Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Ancylostoma caninum SS/LS cDNA PCR products of
size >400 nucleotides containing SL1 on the 5' end and
oligo(dT) on the 3' end were non-directionally cloned
into PCRIT-TOPO(Invitrogen) following the TOPO TA cloning
protocol. Nematodes were provided by Dr. Prema Arasu
(Prema.Arasu@ncsu.edu) of North Carolina State University
in Raleigh, NC."

KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
REFERENCE 1 (bases 1 to 452)
AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,
'C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon
'R.A.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
JOURNAL Unpublished (2000)
COMMENT On Apr 14, 2000 this sequence version replaced gi:7569391.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 736 Std Error: 0.00
Plate: 078 row: E column: 03
Seq primer: TCACACAGGAACAGCATATGAC.
Location/Qualifiers
1. 452
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF078E03ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda zap; Contains a mixture of
internodal stem segments"

BASE COUNT 152 a 94 c 91 g 115 t
ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 452;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
|||||
DB 338 CATTTCGATGACCC 324

RESULT 6
LOCUS TA247H04P 517 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 247H04, forward sequence,
genomic survey sequence.
ACCESSION AL483262
VERSION AL483262.1 GI:11848938
KEYWORDS
SOURCE
ORGANISM Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 517)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREN927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

SOURCE

1..517
Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"

BASE COUNT 116 a 116 c 135 g 150 t

ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
|||||
Db 293 GCGCTTCGATGAAC 307

RESULT 7

LOCUS

AO783856 536 bp DNA linear GSS 03-AUG-1999
DEFINITION HS.2001_A2_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.

ACCESSION AO783856
VERSION AO783856.1 GI:5691480
KEYWORDS GSS.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 536)
Mahaitsa,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahaitsa GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2001 row: K column: 18
Seq Primer: T7
Class: BAC ends
High quality sequence stop: 536.
Location/Qualifiers

TITLE

JOURNAL
MEDLINE
COMMENT

FEATURES

SOURCE

1..536
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2001 Col=18 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-coli DH10B"
BASE COUNT 160 a 124 c 92 g 156 t 4 others

ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaaccc 20
|||||
Db 506 CGCTTCGATGAACCC 520

RESULT 8

LOCUS

TA140G03P 537 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 140g03, forward sequence,
genomic survey sequence.

ACCESSION AL466454
VERSION AL466454.1 GI:11835809
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

1 (bases 1 to 537)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajadream,M.A. and Barrell,B.G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

TITLE

JOURNAL
COMMENT
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

FEATURES

SOURCE

1..537
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="140g03"

BASE COUNT 108 a 120 c 110 g 199 t

ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 537;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
|||||
Db 85 GCGCTTCGATGAAC 99

RESULT 9

LOCUS

TA190A10P 540 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 190a10, forward sequence,
genomic survey sequence.

ACCESSION AL477985
VERSION AL477985.1 GI:11841795
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

ORIGIN

REFERENCE 1 (bases 1 to 540)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Majandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.
 FEATURES
 source Location/Qualifiers
 1..540
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="190a10"
 BASE COUNT 177 a 118 c 126 g 119 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 540;
 Best Local Similarity 100.0%; Pred. NO. 41;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 ggcgttcgatgaac 18
 ||||||||||||
 DB 325 GCGCTTCGATGAC 311
 RESULT 10
 BH615799 631 bp DNA linear GSS 28-JAN-2002
 LOCUS BMAC304F01SP6_P5U Brugia malayi Genomic Bac Library 3 Brugia
 DEFINITION malayi genomic, DNA sequence.
 ACCESSION BH615799
 VERSION BH615799.1 GI:18380487
 KEYWORDS GSS.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Sphurida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 631)
 Whittton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
 J., Guillano, D., Statko, B. and Blaxter, M.
 Genome survey sequences from the human parasitic nematode Brugia
 malayi
 JOURNAL Unpublished (2000)
 COMMENT Contact: Blaxter M.
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3JF, UK
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire
 Whittton and Dr Mike Quail. The sequence was generated by The
 Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
 collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
 Edinburgh, UK.
 Seq primer: SP6 (ATTAGGTGACTATAG)
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..631
 /organism="Brugia malayi"
 /strain="TRS"
 /db_xref="taxon:6279"
 /clone_lib="Brugia malayi Genomic Bac Library 3"
 /sex="Mixed (male and female)"
 /tissue_type="whole parasite"
 /dev_stage="microfilaria (L1)"
 /note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
 genomic DNA was partially cleaved with Sau3A I and site
 fractionated. 7,392 clones were generated with mean insert
 size ~48 kbp. The library was constructed by Claire
 Whittton, Blaxter Nematode Genetics Lab, University of
 Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
 Unit, The Sanger Centre, Cambridge, UK."
 BASE COUNT 196 a 94 c 142 g 199 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 631;
 Best Local Similarity 100.0%; Pred. NO. 42;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 acggcgcttcgatga 16
 ||||||||||||
 DB 606 ACGGCGTTGATGA 620
 RESULT 11
 BE053145 690 bp mRNA linear EST 07-MAR-2001
 LOCUS GA_Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
 DEFINITION arboreum cDNA clone GA_Ea0002K16f, mRNA sequence.
 ACCESSION BE053145
 VERSION BE053145.2 GI:13244065
 KEYWORDS EST.
 SOURCE Gossypium arboreum.
 ORGANISM Gossypium arboreum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 690)
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
 D., Wood, T.C., Leslie, A. and Wilkins, T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 JOURNAL Unpublished (2000)
 COMMENT On Jun 8, 2000 this sequence version replaced gi:8380201.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TATACGACTCCTATAGG
 High quality sequence stop: 550.
 FEATURES
 source Location/Qualifiers
 1..690
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone="GA_Ea0002K16f"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /tissue_type="Fibers isolated from bolls harvested 7-10
 dpa"
 /lab_host="E. coli"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 169 a 132 c 151 g 236 t
 ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 690;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
 |||
 Db 567 GGCCTTCGATGAA 581

RESULT 12
 CENS040YF 1033 bp DNA linear GSS 18-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 073004 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL269530.1 GI:7991421
 VERSION AL269530
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.
 1 (bases 1 to 1033)
 Roest-Crollius,H., Jallou,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billaule,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Unpublished
 2 (bases 1 to 1033)
 Roest-Crollius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 Unpublished
 3 (bases 1 to 1033)
 Genoscope.
 REFERENCE Direct Submission
 AUTHORS Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 JOURNAL This sequence is a single read and was generated as part of a large
 COMMENT scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.
 FEATURES
 source
 1. 1033
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone_lib="G"
 /note="Genoscope sequence ID : CDBG073BH02LP1-end : T7"

BASE COUNT 270 a 222 c 276 g 261 t 4 others

ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 1033;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 cggcgttcgatgaac 17
 |||
 Db 460 CGGCCTTCGATGAA 446

RESULT 13
 BM007170 1218 bp mRNA linear EST 30-OCT-2001
 LOCUS 60361493371 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420616 3',
 DEFINITION mRNA sequence.
 COMMENT BM007170

VERSION BM007170.1 GI:16521524
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 1218)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs@email.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1876 row: a column: 09
 High quality sequence start: 25
 High quality sequence stop: 313.
 Location/Qualifiers
 1. 1218
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5420816"
 /clone_lib="NIH_MGC_110"
 /tissue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;
 Site 2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: This is a NIH_MGC Library."

BASE COUNT 370 a 446 c 244 g 154 t 4 others

ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
 |||
 Db 364 CGTTCGATGAAACC 378

RESULT 14
 AV640031 247 bp mRNA linear EST 15-DEC-2000
 LOCUS AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
 DEFINITION CDNA clone HCL009B04_5', mRNA sequence.
 ACCESSION AV640031 GI:10783359
 VERSION AV640031
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.
 1 (bases 1 to 247)
 Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
 Nakamura,Y. and Tabata,S.
 Generation of expressed sequence tags from low-CO2 and high-CO2
 adapted cells of Chlamydomonas reinhardtii
 DNA Res. 7 (5), 305-307 (2000)
 TITLE JOURNAL
 MEDLINE 20539644
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES

Location/Qualifiers
1..247

/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL024a01.r"
/clone_jlb="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"

BASE COUNT 61 a 79 c 54 g 53 t
ORIGIN

Query Match

Best Local Similarity 70.0%; Score 14; DB 9; Length 247;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
|||||

DB 245 GGC GTTCGATGAA 232

RESULT 15

AV640876/c

LOCUS

AV640876 Chlamydomonas reinhardtii 269 bp mRNA linear EST 15-DEC-2000

DEFINITION

AV640876 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
CDNA clone HCL024a01_r 5', mRNA sequence.

ACCESSION

AV640876
AV640876.1 GI:10784204

VERSION

EST.

KEYWORDS

Chlamydomonas reinhardtii.

SOURCE

Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

ORGANISM

Chlamydomonas reinhardtii.

REFERENCE

1 (bases 1 to 269)
Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
Nakamura, Y. and Tabata, S.

TITLE

Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii

JOURNAL

DNA Res. 7 (5), 305-307 (2000)

COMMENT

Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

FEATURES

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

Location/Qualifiers

1..269

source

/organism="Chlamydomonas reinhardtii"
/strain="C9"

db_xref="taxon:3055"

/clone="HCL024a01.r"

/clone_jlb="Chlamydomonas reinhardtii 5% CO2"

/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:

XhoI; The cDNA library was constructed from cells cultured

in a medium with bubbling air containing 5% carbon

dioxide"

BASE COUNT

65 a 85 c 60 g 59 t

ORIGIN

Query Match

Best Local Similarity 70.0%; Score 14; DB 9; Length 269;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
|||||

DB 254 GGC GTTCGATGAA 241

Search completed: August 7, 2002, 23:12:33
Job time: 11072 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:21 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20
Sequence: 1 tacgcgcgttcgatgaacc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 segs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAA49824	Myobacterium tube
2	20	100.0	20	AAA49826	Myobacterium tube
3	20	100.0	432	AAO61457	M. tuberculosis rpo
4	20	100.0	480	AAA49863	Myobacterium tube
5	20	100.0	620	AAT29126	rpoB gene fragment
6	20	100.0	620	AAT29124	rpoB gene fragment
7	20	100.0	620	AAT29125	rpoB gene fragment
8	20	100.0	970	AAT09676	Myobacterium tube
9	20	100.0	3519	AAH51976	Myobacterium tube

C 10	20	100.0	3534	22	AAH02079	Myobacterium tube
C 11	20	100.0	3853	21	AAA74651	Myobacterium tube
C 12	20	100.0	3853	21	AAH89994	M. tuberculosis rp
C 13	19	95.0	19	17	AAT12096	M. tuberculosis rp
C 14	15	75.0	27	17	AAT09670	Myobacterium tube
C 15	14	70.0	3447	14	AAO51532	M. leprae rpoB gene
C 16	14	70.0	3474	14	AAS51357	Enterococcus faeca
C 17	14	70.0	3624	23	AAS52892	Enterococcus faeca
C 18	14	70.0	6275	24	ABL32551	Human immune syste
C 19	14	70.0	6319	23	ABL18447	Drosophila melanog
C 20	14	70.0	9179	20	AAH13246	Enterococcus faeca
C 21	14	70.0	9728	24	ABL33903	Human immune syste
C 22	14	70.0	29555	23	ABL18446	Drosophila melanog
C 23	13	65.0	58	22	AAF61643	Lactobacillus case
C 24	13	65.0	234	17	AAT13651	ACNPV ORF 43, resi
C 25	13	65.0	351	22	AAF61568	Lactobacillus case
C 26	13	65.0	383	19	AAV04618	Flea aminopeptidas
C 27	13	65.0	383	22	AAC90900	Flea aminopeptidas
C 28	13	65.0	421	23	AAS94185	DNA encoding novel
C 29	13	65.0	537	19	AAV04619	DNA encoding novel
C 30	13	65.0	537	22	AAC90901	Flea aminopeptidas
C 31	13	65.0	667	22	AAF71326	Corynebacterium g1
C 32	13	65.0	1086	22	AAF27618	Mevalonate pathway
C 33	13	65.0	1227	23	AAS87269	DNA encoding novel
C 34	13	65.0	1242	23	ABL22843	Drosophila melanog
C 35	13	65.0	1261	18	AAV74720	Staphylococcus aur
C 36	13	65.0	1326	22	AAH68314	C glutamicum codin
C 37	13	65.0	1407	22	AAH53127	S. epidermidis ope
C 38	13	65.0	1473	21	AAC48699	Arabidopsis thalia
C 39	13	65.0	1475	21	AAC32775	Arabidopsis thalia
C 40	13	65.0	1938	22	AAF89013	Murine FATP1 codin
C 41	13	65.0	2109	23	AAS92952	DNA encoding novel
C 42	13	65.0	2192	23	AAS92789	DNA encoding novel
C 43	13	65.0	2222	20	AAZ38124	Human FATP variant
C 44	13	65.0	2470	23	AAH594186	DNA encoding novel
C 45	13	65.0	2870	23	ABL26802	Drosophila melanog

ALIGNMENTS

RESULT 1
ID AAA49824 standard: DNA: 20 BP.
AAA49824:
XX
AC
XX
XX
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX
KW Antibiotic resistance: rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999: 99WO-CA01177.
XX
XX 11-DEC-1998: 98US-0111794.
XX
XX (VISI-) VISIBLE GENETICS INC.
XX
XX Shipman R:
XX WPI: 2000-431611/37.
XX
XX Method for the detection and characterization of Mycobacterium
XX tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the *Mycobacterium tuberculosis*
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 1 tacggcgcttcgatgaacc 20
XX
RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE *Mycobacterium tuberculosis* rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PE 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of *Mycobacterium*
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 1 tacggcgcttcgatgaacc 20
XX
RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA; 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE *M. tuberculosis* rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PE 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
XX
PR 30-APR-1992; 92US-0875940.
XX
PR 14-AUG-1992; 92US-0929206.
XX
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASST-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI: 1993-368812/46.
DR P-PSDB; AAR51372.
XX

PT Rapid detection of antibiotic resistance in *Mycobacteria* - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2: Fig 13: 97pp: English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant *Mycobacterium leprae* strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from *M. tuberculosis* (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 428 TAGCGCGTTTCGATGAACCC 409

RESULT 4
AAAA9863/C
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE *Mycobacterium tuberculosis* rpoB gene (rifampin resistance).
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS *Mycobacterium tuberculosis*.
XX
FH Key location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag= a
FT /*note= "primer of AAA49823"
FT 372..391
FT /*tag= b
FT /*note= "primer of AAA49824"
ET
XX
XX WO200036142-A1.
XX
XX
XX 22-JUN-2000.
XX
XX PD 10-DEC-1999; 99WO-CA01177.
XX
XX PF 11-DEC-1998; 98US-0111794.
XX
XX PR 11-DEC-1998; 98US-0111794.
XX
XX PA (VISI-) VISIBLE GENETICS INC.
XX
XX Shipman R;
PI
XX
XX WPI; 2000-431611/37.
XX
XX
XX Method for the detection and characterization of *Mycobacterium*
XX tuberculosis with antibiotic resistance in a sample -
XX
XX
XX Disclosure; Page 5; 43pp: English.
XX
XX The present sequence is that of the *Mycobacterium tuberculosis*
XX rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
XX cycle sequencing primers (see AAA49823-62) are used for the detection
XX and analysis of antibiotic resistance-associated mutations in
XX defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
XX (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 451 TAGCGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/C
ID AAT29126 standard; DNA; 620 BP.
XX
XX AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
XX
DE rpoB gene fragment (mutant) from *Mycobacterium tuberculosis*.
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; *Mycobacterium*; Shigella;
XX Staphylococcus; identification; detection; ds.
XX
XX
XX *Mycobacterium tuberculosis*.
XX
XX
XX WO9615267-A1.
XX
XX PD 23-MAY-1996.
XX
XX PF 09-NOV-1995; 95WO-US14673.
XX
XX PR 30-AUG-1995; 95US-0520946.
XX
XX PR 09-NOV-1994; 94US-0337164.
XX
XX PR 09-MAR-1995; 95US-0402601.
XX
XX PR 07-JUN-1995; 95US-0484956.
XX
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamchev VI;
XX Oldenburg MC, Olive DM;
XX
XX WPI; 1996-259862/26.
XX
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection
XX esp. in human p53 gene, to identify strains of microorganisms and
XX viruses
XX
XX
XX Example 33; Page 306; 43pp: English.
XX
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
XX selected from the group consisting of cleavage (Rm) DN enzyme,
XX Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
XX polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
XX Ccd1/Rad10 complex. The nucleic acid substrate is preferably an
XX oligonucleotide containing a human p53 gene sequence or
XX alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6

AAT29124/C
ID AAT29124 standard; DNA; 620 BP.

XX
AC AAT29124;

DT 02-DEC-1996 (first entry)

XX
DE rpoB gene fragment from Mycobacterium tuberculosis.

XX
KM P53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; Identification; detection; ds.

XX
OS Mycobacterium tuberculosis.

XX
PN W09615267-A1.

XX
PD 23-MAY-1996.

XX
PF 09-NOV-1995; 95WO-US14673.

XX
PR 30-AUG-1995; 95US-0520946.

XX
PR 09-NOV-1994; 94US-0337164.

XX
PR 09-MAR-1995; 95US-0402601.

XX
PR 07-JUN-1995; 95US-0484956.

XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX
PI Oldenburg MC, Olive DM;

XX
DR WPI; 1996-259862/26.

XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection

XX
PT esp. in human p53 gene, to identify strains of microorganisms and

XX
PT viruses

XX
PS Example 33; Page 305; 433pp; English.

XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 7

AAT29125/C
ID AAT29125 standard; DNA; 620 BP.

XX
AC AAT29125;

DT 02-DEC-1996 (first entry)

XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.

XX
KM P53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; Identification; detection; ds.

XX
OS Mycobacterium tuberculosis.

XX
PN W09615267-A1.

XX
PD 23-MAY-1996.

XX
PF 09-NOV-1995; 95WO-US14673.

XX
PR 30-AUG-1995; 95US-0520946.

XX
PR 09-NOV-1994; 94US-0337164.

XX
PR 09-MAR-1995; 95US-0402601.

XX
PR 07-JUN-1995; 95US-0484956.

XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX
PI Oldenburg MC, Olive DM;

XX
DR WPI; 1996-259862/26.

XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection

XX
PT esp. in human p53 gene, to identify strains of microorganisms and

XX
PT viruses

XX
PS Example 33; Page 305-306; 433pp; English.

XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
 CC method is used for detecting mutation in the human p53 gene; for
 CC identifying strains of microorganisms, especially bacteria selected
 CC from the group of members of the genera Campylobacter,
 CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
 CC The method may also be used for the identification of viruses,
 CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
 CC (SIV). Two primers (AAT9122, AAT9123) were used to amplify a 620 bp
 CC region of the Mycobacterium tuberculosis rpoB gene, which, when
 CC mutated is associated with rifampin resistance. The 620 bp region
 CC amplified spans both the H451Y and S456L mutations. The amplified
 CC fragments are given in AAT9124 (wild type) and AAT9125-26
 CC (mutant sequences).

CC Sequence 620 BP: 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgataaaccc 20
 DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 8

AAT09676/C
 ID AAT09676 standard; DNA: 970 BP.

XX AAT09676;

XX 15-OCT-1996 (first entry)

DE Mycobacterium tuberculosis rpoB gene DNA sequence.

XX Tuberculosis; disease diagnosis: oligonucleotide; DNA primer; PCR;
 KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers

FT primer_bind 10..27 /tag= a

FT primer_bind 226..243 /note= "primer FENLFF"

FT primer_bind 226..240 /tag= b

FT primer_bind 226..240 /note= "primer DDIDL"

FT primer_bind 338..364 /tag= c

FT primer_bind 338..364 /note= "primer DDIDL"

FT primer_bind 348..373 /tag= d

FT primer_bind 348..373 /note= "primer rpo95"

FT primer_bind 354..373 /tag= e

FT primer_bind 354..373 /note= "primer rpo105"

FT primer_bind 372..373 /tag= f

FT primer_bind 372..373 /note= "primer KY290"

FT primer_bind 433..434 /tag= g

FT primer_bind 433..434 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 438 /tag= h

FT primer_bind 438 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 468..469 /tag= i

FT primer_bind 468..469 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 486 /tag= j

FT primer_bind 486 /note= "M. tuberculosis signature nucleotide"

FT /tag= k

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind 501 /tag= l

FT primer_bind 501 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 516 /tag= m

FT primer_bind 516 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 516..535 /tag= n

FT primer_bind 516..535 /note= "primer rpo273"

FT primer_bind 525 /tag= o

FT primer_bind 525 /note= "M. tuberculosis signature nucleotide"

FT primer_bind 525..541 /tag= p

FT primer_bind 525..541 /note= "primer KY292"

FT primer_bind 536..562 /tag= q

FT primer_bind 536..562 /note= "primer rpo293"

FT primer_bind 640..666 /tag= r

FT primer_bind 640..666 /note= "primer rpo397"

FT primer_bind 952..966 /tag= s

FT primer_bind 952..966 /note= "primer NMORQ-1"

FT primer_bind 952..966 /tag= t

FT primer_bind 952..966 /note= "primer NMORQ-2"

XX WO9533074-A1.

XX 07-DEC-1995.

XX 26-MAY-1995; 95WO-US06790.

XX 26-MAY-1994; 94US-0250030.

XX (HOFF) HOFFMANN LA ROCHE INC.

XX (MAYO-) MAYO FOUNDATION.

XX felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;

XX Young KKY;

XX WPI: 1996-030581/03.

XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA

XX with a primer set that targets portions of the gene encoding rpoB.

XX Disclosure: Fig.3; 54pp; English.

XX This oligonucleotide DNA primer is specific for Mycobacterium

XX tuberculosis, and may be used to amplify a sample DNA by targeting

XX a portion of the gene encoding rpoB. The 1st several bases comprise a

XX nonhybridizing tail consisting of filler bases followed by

XX a restriction site incorporated to facilitate cloning using the

XX amplicon at a later date, if desired. The remaining bases hybridize

XX to bacterial rpoB DNA. The method provides for the detection of M.

XX tuberculosis and the concurrent determination of its drug

XX susceptibility, particularly to rifampin. The method can provide

XX often greater than 95% sensitivity and 100% specificity. The

XX biological sample is a fluid or tissue sample from a human.

XX Sequence 970 BP: 182 A; 302 C; 330 G; 156 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 970;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgataaaccc 20
 DB 671 TACGGCGTTTCGATGAACCC 652

```

RESULT 9
AAH51976/c
ID AAH51976 standard; DNA: 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KM Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI: 2001-329193/34.
XX
XX P-PSDB; AAG81125.
XX
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
XX involves providing algorithm that analyzes a functional relationship
XX between nucleotide or polypeptide sequences, and comparing the
XX sequences
XX
XX
XX Disclosure: Page 68-69; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241. Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX algorithm capable of analysing a functional relationship between
XX nucleotide and polypeptide sequences. The method is useful for
XX characterising the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3519;
XX Best Local Similarity 100.0%; Pred. No. 0.0064;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 tacgagcttcgatgacc 20
XX ||||||||||||||||
XX DB 1529 TACGGCGTTTCGATGAACCC 1510
XX
XX
XX RESULT 10
XX AAH02079/c
XX ID AAH02079 standard; DNA: 3534 BP.
XX
XX AC AAH02079;
XX
XX
XX 24-JUL-2001 (first entry)
XX

```

```

XX
XX Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitical;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial;
XX vaccine; primer; ds.
XX
XX
XX OS Mycobacterium tuberculosis.
XX
XX PN W0200123604-A2.
XX
XX PD 05-APR-2001.
XX
XX PF 28-SEP-2000; 2000WO-CA01150.
XX
XX PR 28-SEP-1999; 99CA-2283458.
XX PR 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
XX Picard FJ, Roy PH;
XX
XX WPI: 2001-245006/25.
XX
XX
XX Nucleic acid sequences are used to generate universal probes and
XX primers which can be used to identify and detect the presence of algal,
XX archaeal, bacterial, fungal and parasitical species in a test sample -
XX
XX
XX Disclosure: Page 1478-1479; 1580pp; English.
XX
XX The present invention describes a method for generating a repertoire of
XX nucleic acids of tuf, fus, atpd and/or recA genes from which probes
XX and/or primers are derived. The method comprises amplifying the nucleic
XX acids of determined algal, archaeal, bacterial, fungal and parasitical
XX species with a combination of defined primer pairs. The method can be
XX used for producing probes and/or primers for detecting one or more
XX related microorganisms e.g. algae, archaea, bacteria, fungi and
XX parasites, for universal detection and for specific and ubiquitous
XX detection and identification of an algal, archaeal, bacterial, fungal
XX and parasitical species, genus, family and group. A nucleic acid (1)
XX obtained using the method of the invention can be used for the universal
XX detection of any bacterium, fungus or parasite in a sample and for the
XX detection of at least one antimicrobial agent resistance gene or at
XX least one toxin gene. hexA nucleic acids are used for the specific and
XX ubiquitous detection and for identification of Streptococcus pneumoniae.
XX (1) can be used to design a therapeutic agent which is effective against
XX microorganisms. Microbial species or genus or family or phylum or group
XX which can be detected include Abiotrophia adiacens, Bordetella coli,
XX Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,
XX Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
XX provides faster results than substrate specificity tests as results can
XX be determined in an hour and improved accuracy is also achieved.
XX AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX which are given in the exemplification of the present invention.
XX
XX Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3534;
XX Best Local Similarity 100.0%; Pred. No. 0.0064;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 tacgagcttcgatgacc 20
XX ||||||||||||||||
XX DB 1547 TACGGCGTTTCGATGAACCC 1528
XX
XX
XX RESULT 11
XX

```

```

AAA74651/C
ID AAA74651 standard; DNA; 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
KM rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||
|||||

RESULT 12
ID AAA89994 standard; DNA; 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KM RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
PI

```

```

PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

```

```

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||
|||||

RESULT 13
ID AAT12096 standard; DNA; 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
KM determination; amplification; tuberculosis; rpoB; fragment;
KM primer; differential; hybridisation; pattern; rifampicin;
KM rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machteldinckx L, Portela F;

```

```

PI Rosau R;
XX WPI: 1996-040250/04.
XX
XX Probes and primers for determ. of antibiotic resistance spectrum of
XX Mycobacterium, opt. coupled with species identification - from
XX different patterns of hybridisation with rpoB gene
XX
XX Claim 22; Page 39; 69pp; English.
XX
XX The antibiotic resistance spectrum (ARS) of a mycobacterium can be
XX determined by amplifying the relevant part of the antibiotic
XX resistance gene, i.e. the M. tuberculosis rpoB gene fragment
XX amplified using the primer set AAT12091-98, hybridising it with at
XX least 1 rpoB gene probe, detecting the hybrids formed and
XX inferring the ARS, and opt. the spp., from the differential
XX hybridisation patterns. The method is partic. useful for the
XX detection of rifampicin and/or rifabutin resistance in M. leprae
XX or M. tuberculosis, and mycobacterial spp. identification. The
XX method is rapid and reliable and provides simultaneous determ.
XX of ARS and spp. identity.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other:

Query Match          95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgttcgatgaacc 19
   |||
Db 1 taccgcgttcgatgaacc 19

RESULT 14
AAT09670
ID AAT09670 standard; DNA; 27 BP.
XX
XX AAT09670;
XX
XX 15-OCT-1996 (first entry)
XX
XX Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
XX Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
XX polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
XX Synthetic.
XX
XX W09533074-A1.
XX
XX 07-DEC-1995.
XX
XX 26-MAY-1995; 95WO-US06790.
XX
XX 26-MAY-1994; 94US-0250030.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Feljmele TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX Young KKY;
XX
XX WPI: 1996-030581/03.
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Claim 9; Page 39; 54pp; English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The method provides for the

```

```

CC detection of M. tuberculosis and the concurrent determination of its
CC drug susceptibility, particularly to rifampicin. The method can
CC provide often greater than 95% sensitivity and 100% specificity.
CC The biological sample is a fluid or tissue sample from a human.
XX
SQ Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other:

Query Match          75.0%; Score 15; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 8 8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
   |||
Db 1 cgttcgatgaacc 15

RESULT 15
AAQ51532/c
ID AAQ51532 standard; DNA; 3447 BP.
XX
XX AAQ51532;
XX
XX 17-MAY-1994 (first entry)
XX
XX M.leprae rpoB gene.
XX
XX rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
XX mutant; ss.
XX
XX Mycobacterium leprae.
XX
XX Key Location/Qualifiers
XX CDS 1..3447
XX FT /*tag= a
XX FT /note= "rifampicin-sensitive; in resistant
XX FT strains the Ser codon (TCG at
XX FT nucleotides 1273-1275) is often mutated
XX FT to a Phe, Met or esp. Leu codon"
XX
XX W09322454-A.
XX
XX 11-NOV-1993.
XX
XX 30-APR-1993; 93WO-EP01063.
XX
XX 17-SEP-1992; 92FR-0011098.
XX 30-APR-1992; 92US-0875940.
XX 14-AUG-1992; 92US-0929206.
XX 16-APR-1993; 93FR-0004545.
XX
XX (ASSI-) ASSISTANCE PUBLIQUE.
XX (INSP ) INST PASTEUR.
XX (MEDT-) MEDICAL RES COUNCIL.
XX (UTBE-) UNIV BERNE.
XX (UTPA-) UNIV CURIE PARIS VI P & M.
XX
XX Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX Young D, Zhang Y;
XX
XX WPI: 1993-368812/46.
XX P-PSDB; AAR43671.
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
XX isoniazid, rifampicin or streptomycin resistance in tuberculosis
XX by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Fig 12; 97pp; English.
XX
XX PCR amplification was used to obtain rpoB genes from rifampicin-
XX resistant Mycobacterium leprae strains. A comparison with the
XX sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
XX mutations in the region encoding amino acids 400-450. A common

```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP: 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 gtttcgatgaacc 20
|||||
Db 1448 GTTCGATGAACCC 1435

Search completed: August 8, 2002, 00:01:22
Job time: 7611 sec

119

This Page Blank (uspto)

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
XX AAT29124;
AC
XX
DT 02-DEC-1996 (first entry)

DE rpoB gene fragment from Mycobacterium tuberculosis.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX Staphylococcus; identification; detection; ds.

XX Mycobacterium tuberculosis.

XX W09615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95WO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX Oldenburg MC, Olive DM;

XX WPI; 1996-259862/26.

XX Example 33; Page 305; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
XX AAT29125;
AC
XX
DT 02-DEC-1996 (first entry)

DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX Staphylococcus; identification; detection; ds.

XX Mycobacterium tuberculosis.

XX W09615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95WO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX Oldenburg MC, Olive DM;

XX WPI; 1996-259862/26.

XX Example 33; Page 305-306; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

PT Rapid detection of antibiotic resistance in *Mycobacteria* - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant *Mycobacterium leprae* strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from *M. tuberculosis* (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCCTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.

XX
AC AAA49863;

DT 25-SEP-2000 (first entry)

DE *Mycobacterium tuberculosis* rpoB gene (rifampin resistance).

KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.

XX
OS *Mycobacterium tuberculosis*.

XX
FH Key Location/Qualifiers
FT primer_bind /tag= a
complement(41..60)

FT primer_bind /note= "primer of AAA49823"
372..391
/tag= b
/note= "primer of AAA49824"

XX
PN W0200036142-A1.

PD 22-JUN-2000.

XX
PF 10-DEC-1999; 99WO-CA01177.

XX
PR 11-DEC-1998; 98US-0111794.

XX
PA (VISI-) VISIBLE GENETICS INC.

XX
PI Shipman R;

DR WPI; 2000-431611/37.

XX
PT Method for the detection and characterization of *Mycobacterium*
PT tuberculosis with antibiotic resistance in a sample -

XX
PS Disclosure; Page 5; 43pp; English.

XX
CC The present sequence is that of the *Mycobacterium tuberculosis*
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 451 TACGGCCTTCGATGAACCC 432

RESULT 5
AAT29126/c

ID AAT29126 standard; DNA; 620 BP.

XX
AC AAT29126;

DT 02-DEC-1996 (first entry)

DE rpoB gene fragment (mutant) from *Mycobacterium tuberculosis*.

XX
KW p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; *Mycobacterium*; Shigella;

XX
KW Staphylococcus; identification; detection; ds.

XX
OS *Mycobacterium tuberculosis*.

XX
PN W09615267-A1.

PD 23-MAY-1996.

XX
PF 09-NOV-1995; 95WO-US14673.

XX
PR 30-AUG-1995; 95US-0520946.

XX
PR 09-NOV-1994; 94US-0337164.

XX
PR 09-MAR-1995; 95US-0402601.

XX
PR 07-JUN-1995; 95US-0484956.

XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX
PI Oldenburg MC, Olive DM;

XX
DR WPI; 1996-259862/26.

XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses

XX
PS Example 33; Page 306; 433pp; English.

XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are


```
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), embA (ethambutol), pncA (pyrazinamide), gyrA
CC (chlorofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
DB 1 tacggcgcttcgatgaacc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA: 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
```

```
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), embA (ethambutol), pncA (pyrazinamide), gyrA
CC (chlorofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
DB 1 tacggcgcttcgatgaacc 20

RESULT 3
AAO61457/C
ID AAO61457 standard; DNA: 432 BP.
XX
AC AAO61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M. tuberculosis rpoB gene fragment.
XX
KM rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP-) INST PASTEUR.
PA (MEDIT-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNIE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:25 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: us-09-786-105-4

Perfect score: 20
Sequence: 1 tacggcgcttcgatgaacc 20

Scoring table:

OLIGO_NUC
Gap 60.0 , Gapext 60.0

Searched: 1736436 segs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

N.Geneseq_032802:*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	21	AAA49824
2	20	100.0	20	14	AAA49826
3	20	100.0	432	21	AAO61457
4	20	100.0	480	21	AAA49863
5	20	100.0	620	17	AAAT29126
6	20	100.0	620	17	AAAT29124
7	20	100.0	620	17	AAAT29125
8	20	100.0	970	17	AAAT09676
9	20	100.0	3519	22	AAH51976

C	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
C	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
C	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
C	13	19	95.0	19	17	AAT12096	Mycobacterium tube
C	14	15	75.0	27	17	AAT09670	M. leprae rpoB gene
C	15	14	70.0	3447	14	AAQ51532	Enterococcus faeca
C	16	14	70.0	3474	23	AAAS1357	Enterococcus faeca
C	17	14	70.0	3624	23	AAAS2892	Human immune syste
C	18	14	70.0	6275	24	ABL22551	Human immune syste
C	19	14	70.0	6319	23	ABL18447	Enterococcus faeca
C	20	14	70.0	9179	20	AAK13246	Enterococcus faeca
C	21	14	70.0	9728	24	ABL33903	Human immune syste
C	22	14	70.0	29555	23	ABL18446	Drosophila melanog
C	23	13	65.0	58	22	AAAF1643	Lactobacillus case
C	24	13	65.0	234	17	AAAT13651	ACNPV ORF 43, res1
C	25	13	65.0	351	22	AAAF1568	Lactobacillus case
C	26	13	65.0	383	19	AAV04618	Flea aminopeptidas
C	27	13	65.0	383	22	AAAC9090	Flea aminopeptidas
C	28	13	65.0	421	23	AAAS94185	DNA encoding novel
C	29	13	65.0	537	19	AAV04619	Flea aminopeptidas
C	30	13	65.0	537	22	AAAC90901	Flea aminopeptidas
C	31	13	65.0	667	22	AAAF1326	Corynebacterium gl
C	32	13	65.0	1086	22	AAAF27618	Mevalonate pathway
C	33	13	65.0	1227	23	AAAS87269	Drosophila melanog
C	34	13	65.0	1242	23	ABL22843	Staphylococcus aur
C	35	13	65.0	1261	18	AAV74720	C glutamincum codin
C	36	13	65.0	1326	22	AAH68314	S. epidermidis ope
C	37	13	65.0	1407	22	AAH53127	Arabidopsis thalia
C	38	13	65.0	1473	21	AAAC48699	Murine FARP1 codin
C	39	13	65.0	1475	21	AAAC32775	DNA encoding novel
C	40	13	65.0	1938	22	AAAF89013	DNA encoding novel
C	41	13	65.0	2109	23	AAAS92952	Human FARP variant
C	42	13	65.0	2192	23	AAAS92789	DNA encoding novel
C	43	13	65.0	2222	20	AAAS38124	Drosophila melanog
C	44	13	65.0	2470	23	AAAS94186	
C	45	13	65.0	2870	23	ABL26802	

ALIGNMENTS

RESULT	ID	AAA49824	standard; DNA; 20 BP.
XX	XX	AAA49824;	
AC	XX		
DF	XX	25-SEP-2000	(first entry)
DE	XX		
XX	XX		Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
KW	XX		Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KM	XX		ss.
OS	XX		Mycobacterium tuberculosis.
XX	XX		
PN	XX		WO200036142-A1.
PD	XX		22-JUN-2000.
PF	XX		10-DEC-1999; 99WO-CA01177.
PR	XX		11-DEC-1998; 98US-0111794.
PA	XX		(VIST-) VISIBLE GENETICS INC.
PI	XX		Shipman R;
XX	XX		
DR	XX		WPI; 2000-431611/37.
PT	XX		Method for the detection and characterization of Mycobacterium
PT	XX		tuberculosis with antibiotic resistance in a sample -

Thu Aug 8 09:35:17 2002

us-09-786-105-4.oli.rge

Page 8

```
/product="Ap endonuclease, family 2"
/db_xref="GI:13880221"
/translation="MLIGSHVSPDPLAAAEAGAVYQIFLGNPSQWAKPRDDAA
ALKAATPLIVHAPYLINLASANNRVRITSRLLOETCAAADIGAAYIGHGHAD
DNDIDGFORWKALDLLETVEYVLENTAGSGHAAARRDPTARLMDYIGDHGIFC
LPTCHWAGAGEALTDADVDRIKATGRIDIVHCNDSDEAGSGDRHANLNGSGIDBDL
LVAAVKAAGAPVCEFAADQGRKDDIAFLBERTGS"
10957..11799
/gene="MT0700"
10957..11799
/gene="MT0700"
/note="similar to GB:U00012 PID:466863; identified by
sequence similarity; putative"
/codon_start=1
/translation_table=11
/product="hydrolase/esterase, putative"
/protein_id="AAK4925.1"
/db_xref="GI:13880222"
/translation="MLRVAIILAAVLAFAAGSGGTRLAAGFGNSVHTLDVAGAR
SVRLKPVGIPSPAPLVVMHGGFGSAKOERSYGMDELADSEKFLVAYPDGYHMAN
ANGGCCGCRARCGVDIGFVRVAVDIANNVSIDPARVYTGMSGATISYTLACNT
STFAIGVSGTOLDPCQSPRPVSVIHIGTADPLVYHGGPGAGFRIDGPPVDLN
AFWREYVRCGALDTTEGPTVTSATCADNRVLLITVDAGHWPESFATQTLMREFA
AHR"
11859..13487
/gene="MT0701"
11859..13487
/gene="MT0701"
/note="similar to SP:P33224 GB:I20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
putative"
/codon_start=1
/translation_table=11
/product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK4926.1"
/db_xref="GI:13880223"
/translation="MSDTHVITNQVPLENYPASSPVILIALIOEGGOWGLDEVNEY
GAISASCOAORMGELADRNRIILHTDAGYRVDEVEYDPAVYHELMRTALTGHMAAP
WADDRGAHVRAKTSWTEVERGHICPISMTAVVPAALYNSELAAYVEPLTSREY
DPELRPATRKAGITAGMSWTEKOGSDVRGTOATPNADGSYSLTGKHKFTSAPKCD
ITLVLAQAPDGLSCFLIPRYLPDGTNRMPLORKDKLGNHANSSEVEYDGAVALIV
GEEGRGVPITIEVNVNLTSLDCAIGSATSMRTGLTRAVHQAHRKAFGAYLIDPLMIN
VLADLVEAEATIVAMRNAGATDNVANGNETELRLRIGLIAAKYWCCKRSTAHAE
ALECLGNGYVEDSGMPRLYREAPLMGIMWGSNGSALDTLRAMATRPACVEYLFDEL
ARSAAGDPRLDGVERLRLPQLDITIGVARKIADICLALQGSLLVRHGPVAVAE
FLATRLGCGMGAGYGTMPAGLDLAPILERALVKG"
13498..14436
/gene="MT0702"
13498..14436
/gene="MT0702"
/note="similar to GP:3885480; identified by sequence
similarity; putative"
/codon_start=1
/translation_table=11
/product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK4927.1"
/db_xref="GI:13880224"
/translation="MTHTAPVDVDNLTMTYFVPTGRIARTFNPPEKNAITADPPL
ELSAIVERRADLDPCVHIVILVSGREGFCAGFDLSATRESSSTGGGAGYGTIVDGKT
QAVNHLPNQWMDPMIDYQMSRFRVGRFASLMHADKPTVVKIHGYCVAGGTIDIALHADQ
VIAADAKIGYPTRWGVAPAGLMAHRLDQRAKRLFTGDCITGQAAMWGLAVEA
PEPADLDERTERLVARIAALPVNQLINVKLALNSALIQGVATSRMVSIVFDGAARHT
PEGHAFVADAVEHGFDAVRRDEPFGDYGRQASRV"
14439..15161
/gene="MT0703"
14439..15161
/gene="MT0703"
/note="identified by Glimmer2; putative"
/codon_start=1
/translation_table=11
/product="hypothetical protein"
```

```
Query Match          100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcggttcgatgaacc 20
|||||
Db 1709 TACGGCGTTTCGATGAACCC 1690
```

Search completed: August 7, 2002, 23:49:04
Job time: 9218 sec

translation="MDVNFDELRLGICLATADIROMSYGEVKKPPTINRYIKPEKD
GLCEKIFGPTDMCEYCGKYRKVRKRGICICRGCVEYTRAKVRREMRGHITLAPVT
HIMYGVPSRLGYLLDAPKLEIKITFYAAVYITSVDEMRHNEL"

BASE COUNT 969 a 1534 c 1691 g 890 t

Query Match 100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 2611 TACGGCGCTTCGATGAACCC 2592

RESULT 15
AE006964 19352 bp DNA linear BCT 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
DEFINITION complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS Mycobacterium tuberculosis CDC1551.
SOURCE Mycobacterium tuberculosis CDC1551
ORGANISM Bacteria: Firmicutes: Actinobacteriia: Actinobacteridae:
Actinomycetales: Corynebacteriaceae: Mycobacteriaceae:
Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 19352)
AUTHORS Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 19352)
AUTHORS Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
FEATURES
source
1. 19352
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
/db_xref="taxon:83331"
/note="clinical strain"
163. 3699
/gene="MT0695"
163. 3699
/gene="MT0695"
/note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
PID:149992; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK44921.1"
/db_xref="GI:13880218"

gene
CDS
163. 3699
/gene="MT0695"
/note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
PID:149992; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK44921.1"
/db_xref="GI:13880218"

gene
CDS
3744. .7694
/gene="MT0696"
3744. .7694
/gene="MT0696"
/note="similar to SP:P37871; identified by sequence
similarity; putative"
/transl_table=1
/codon_start=1
/product="DNA-directed RNA polymerase, beta-prime subunit"
/protein_id="AAK44922.1"
/db_xref="GI:13880219"

translation="MDVNFDELRLGICLATADIROMSYGEVKKPPTINRYIKPEKD
GLCEKIFGPTDMCEYCGKYRKVRKRGICICRGCVEYTRAKVRREMRGHITLAPVT
HIMYGVPSRLGYLLDAPKLEIKITFYAAVYITSVDEMRHNELSTLPAEAVERK
AVBDRGELSEARAKLEADLAELAEAGADARAKRYRVDGEREMRIRBPAQREIDR
LEDIMSTFTKLPARKOLVDENLREIDRYGEYTGMAESIOKILENDIDAEAS
LRDIYRNGKQCKTRAKRLKVAAPQSGNSPMGWLDVAVPYPLPRMWOLOGGR
FATSDLDLIRVIRNNRLRLIDLCAPETIYNNKRMJESYDALFDNGRGRPT
GPNRPLKLSLIDLKQGRFRONLGRVDYSGRSYIVGPOLKHQCCUPLMALE
LFRPFWKRLVDLNNHONISAKRMWRORPOVWDVEVYIAEPVLIRAPTLRLIG
IOAPEPLVEGKALOLHPLVCEAFNAPDGDMAVHILPSAEQAERILMLSNNTL
SPASGRPLAMPDMDVGLYLTVEYEDGEPDOPASGDHPETGVSSPAEAMADR
GVTSVRKTRIRLTOLPBPVEITELELGEKMGDGMMAETTLRWMEMLPIYGP
FVNQMKKKVQAAITNDLARTPWITVAAGVYDKADGFTWATRSQTVGALMEVLP
RKEEILHYERADKVEKFORGLANDERNEALVEMKATDEVGALKEHFPDNP
IITIVDSGATNGFTQTRLAMKGLVTPNGEFTIPRVKSPFREGVLVLYFTNTGA
RKLADALRTADSGYLTRLRVDSQVIVREHCCPYRKSIVVELARADGTLIRBP
YIETSAVARTLGTAVDEAGNIVVERGODIPEDIALLAAGITOVKRSVLTCATST
GVCAATCYGRSMATGKLVDIGEAVGIVAOSIGERGQTLTRDTHFGGGEVYDKISKRORLV
VOELFERVRRGRKAPIDVYGRVLEGERFYKTTIYDGGGEVYDKISKRORLV
FKHDKSERIVSDSDHVEVGOQLMEGSADEPHEVIRVOPREVOHILVROEYRRAO
VSHDKHIEVIVRQMLRVTIIDSSTFELPSLIDRAEAEENRRVVAAGGEPAAGR
PVLMTGIRKASATDSWLSAASFQETTVLTDAAINCRSDKINLKEVNIIGKLPACT
GINRYNIAVOPTEEARAAVYITPSYEDQYSPDGAATGAAYPLDDYGSXK"

complement(7691. .8065)
/gene="MT0697"
complement(7691. .8065)
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="AAK44923.1"
/db_xref="GI:13880220"

translation="MPSAAATINPGHAMASAMERSGLCEVAGLDROPGEFTADKL
MPDGSRRVPRROADGGIATHYERGGGQSGGQAGVYVQRHMGFPALAMQRLIHH
GEJYONRIQAQFRVFCYCSFT"
complement(8058. .9972)
/gene="MT0698"
/note="This region contains an authentic frame shift and
is not the result of a sequencing artifact; identified by
Glimmer2; putative; conserved hypothetical protein,
authentic frameshift"
10167. .10925
/gene="MT0699"
10167. .10925
/gene="MT0699"
/note="identified by match to PFAM protein family HMM
PF01261"
/codon_start=1
/transl_table=1

Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taagcgcttcgataacc 20
|||||
Db 1547 TACGGCGTTTCGATGACC 1528

RESULT 13

MTU12205/c 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.

ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The rpoB gene of Mycobacterium tuberculosis
Unpublished
2 (bases 1 to 3853)
Imboden, P.
Direct Submission
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland

FEATURES

Source
Location/Qualifiers
1. .3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576. >3853
/gene="rpoB"
576. >3853
/gene="rpoB"
/codon_start=1
/transl_table=1
/product="RNA polymerase beta subunit"
/protein_id="AAA20242.2"
/db_xref="GI:714499"

gene
CDS
/translation="MEEGCLADSRQSKTAASPPSPPOSSNNNSVPGAPNRVSFAKL
REPLEVGLDVQDSEFEMLIGSPRMESAERGDVNPVGLLEVLLELSPIDEDSGS
MSLSFSPRDDVKAPEYDECKDKDMYAAFLPYAEIINNNGEIKSQYPMGDFPM
TEKGTFLINGTERVVSQLVRSRPGVTFDEITDSTDTLSVKYIPSRGAMLEVDVK
RDYGVADIDRRKRPVTVLLKALGWTSEQIVERFSEIMRSTLEKNTGTDEALD
IYRLRPGEPPTKESAQTLLENLFKERYDLAVGRYKVKKLGHLVGEPTSTLL
EEDVATIEVLRLHEGQTMVPGVEVEVDIDHFGNRLRTYVGRKPARSHGTC
MSRMRVRRMTODVEATIPOTLINIRPVAAIKFEGTSQLOPMDONNPLSGIT
HKRLSALGGGSLRERAGLEVDPVHSHGRMCPITTPGPNIGLIGLSISVARVP
EGTEFPYRKVVGVSVDGTVLLADEEDRHVAQAANSPTDADGRFVEPVLVRRKG
EVEVPSSEVDYNDVSRQVAVATANIPELHDDARALMGAMQOAVPLVSEAP
LVGEMELRAIDAATSSSOESGVEVSADYITVMIDNGTRTRYRMRKPARSHGTC
ANOCPIYDADRVREAGVADGCTDGEALGKNLVAIMPENGHYEDAILSNL
VEEDVATIEVLRLHEGQTMVPGVEVEVDIDHFGNRLRTYVGRKPARSHGTC
DIYGVKTPGKEETLPEERLRAIIEFKARREVDTSLKVPHGSGKVGIVRVSERD
EDELPAVNELVRYVAQKRIISDGLAQRHKGKVGIGTILPEEDNPLADGPVUI
ILNTHGVPRRMNTGQILIEHLGMAHSGKGVDAKGVDMARLPDELLEAQPNAIS
TPVFDGAQEAELGSLTLPNRGDVLVDADGKAMLEFDRSGEPFYPYTVGMYIM
KLHLVDDKIHARSTGYSMTIOOPLGKAQFGQGRGEMECWAMQAYGAAYTLOELL
TIKS"

BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taagcgcttcgataacc 20
|||||
Db 2122 TACGGCGTTTCGATGACC 2103

RESULT 14

MSGRPOB 5084 bp DNA linear BCT 13-SEP-1994
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
DEFINITION gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
partial cds.

ACCESSION L27989
VERSION L27989.1 GI:468333
KEYWORDS RNA polymerase beta-subunit; rpoB gene.
SOURCE Mycobacterium tuberculosis (strain RV) DNA.
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
Source
Location/Qualifiers
1. .5084
/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"
1065. 4598
/gene="rpoB"
1065. 4598
/gene="rpoB"
/codon_start=1
/transl_table=1
/evidence="experimental"
/product="RNA polymerase beta-subunit"
/protein_id="AAA21416.1"
/db_xref="GI:468334"

1065. 4598
/gene="rpoB"
1065. 4598
/gene="rpoB"
/codon_start=1
/transl_table=1
/evidence="experimental"
/product="RNA polymerase beta-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:537608"

1065. 4598
/gene="rpoB"
1065. 4598
/gene="rpoB"
/codon_start=1
/transl_table=1
/product="RNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:537608"

partial cds.
AF060353
VERSION GI:3133464
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
AUTHORS
1 (bases 1 to 705)
Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M.,
Drobniowski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
JOURNAL
MEDLINE
Genome Res. 8 (5), 435-448 (1998)
REFERENCE
AUTHORS
2 (bases 1 to 705)
Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M.,
Drobniowski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J.
Direct Submision
TITLE
Submitted (20-APR-1998) Division of Infectious Disease, Affimetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
source
1. 705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:11773"
<1. >705
/gene="rpoB"
<1. >705
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AC38533.1"
/translation="ODVEATTPQTLNIRPVNAIKFEFTSOLSPMDONNPISGTL
HKRSLNLCGCGISREPAIGLEVDVHSHGRCPIETPGSPINGIGLSVYARVP
FGRTETPRKRVGVGVSDLEYITLTADEEDHVAQAQNSPIDAAGRPVPRPVLYRRKG
EVEYVPSVDYDVSDEYVATAMIPLEHDDANLGMAMQAVPLVRSAP
LVGTGMLRAIDAAT"
BASE COUNT 117 a 227 c 250 g 111 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcggttcgatgaacc 20
|||||
Db 331 TACGGCGTTTCGATGAACCC 312
RESULT 10
ARI49128/c 706 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION
Sequence 24 from patent US 6228575.
ACCESSION
ARI49128
VERSION
ARI49128.1 GI:15113719
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS
1 (bases 1 to 706)
Gingeras, T.R., Mack, D., Chee, M.S., Berno, A.J., Stryer, L.,
Ghandour, G. and Wang, C.
TITLE
Chip-based species identification and phenotypic characterization
of microorganisms
JOURNAL
Patent: US 6228575-A 24 08-MAY-2001;
FEATURES
Location/Qualifiers

source 1. 706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcggttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313
RESULT 11
I50706/c 970 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION
Sequence 1 from patent US 5643723.
ACCESSION
I50706
VERSION
I50706.1 GI:2472409
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
AUTHORS
1 (bases 1 to 970)
Persing, D.H., Hunt, J.J., Young, K.K.Y., Fellmlee, T.A., Roberts, G.D.
and Whelan, A.Christian.
TITLE
Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
JOURNAL
Patent: US 5643723-A 1 01-JUL-1997;
FEATURES
source
1. 970
/organism="unknown"
BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcggttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652
RESULT 12
AX111339/c 3534 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION
Sequence 2072 from Patent WO0123604.
ACCESSION
AX111339
VERSION
AX111339.1 GI:13927631
KEYWORDS
SOURCE
Mycobacterium tuberculosis.
ORGANISM
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
AUTHORS
1 (bases 1 to 3534)
Bergeon, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL
Patent: WO 0123604-A 2072 05-APR-2001;
FEATURES
source
1. 3534
/organism="Mycobacterium tuberculosis"
/strain="H37"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 137 from patent US 5843669.
DEFINITION AR062058
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 138 from patent US 5843669.
DEFINITION AR062059
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 139 from patent US 5843669.
DEFINITION AR062060
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 140 from patent US 5843669.
DEFINITION AR062061
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,
DEFINITION

CDS

```

/db_xref="taxon:1773"
<!.>432
/codon_start=1
/transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="AAB59068.1"
/db_xref="GI:149992"
/translation="GNRLRTVIGELIONIRVGMREVRVREMTTODVATPOTL
INIRPVAAIKKEPFGTSQLSQFRDQNNPISGLTKRRLSALGSGISRAGLEVADY
HPSHYGRMCPLEPESGPNIGLSLVYKVPFETPYR"
149
variation /phenotype="rifampicin resistant in association with
mutation 234 G"
188 /replace="c"
variation /phenotype="rifampicin resistant"
191 /replace="c"
variation /phenotype="rifampicin resistant in association with
mutation 203 T"
194 /replace="c"
variation /phenotype="rifampicin resistant"
203 /replace="t"
variation /phenotype="rifampicin resistant"
208 /replace="t"
208 /phenotype="rifampicin resistant"
232 /replace="a"
variation /phenotype="rifampicin resistant"
232 /phenotype="rifampicin resistant"
232 /replace="g"
variation /phenotype="rifampicin resistant"
232 /replace="a"
233 /phenotype="rifampicin resistant"
233 /replace="g"
variation /phenotype="rifampicin resistant"
233 /phenotype="rifampicin resistant"
234 /replace="c"
variation /phenotype="rifampicin resistant"
247 /replace="g"
247 /phenotype="rifampicin resistant"
248 /phenotype="rifampicin resistant"
248 /replace="ca"
variation /phenotype="rifampicin resistant"
248 /replace="g"
variation /phenotype="rifampicin resistant"
254 /replace="t"
254 /phenotype="rifampicin resistant"
variation /replace="c"
BASE COUNT 77 a 140 c 148 g 67 t
ORIGIN

```

Query Match 100.0%; Score 20; DB 1; Length 432;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 |||||
 Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
 AR067448/c 432 bp DNA linear PAT 29-SEP-1999
 LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
 ACCESSION AR067448
 VERSION AR067448.1 GI:5998670
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 432)
 AUTHORS Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and Bodmer,T.
 TITLE Rapid detection of antibiotic resistance in mycobacterium tuberculosis
 JOURNAL Patent: US 5851763-A 59 22-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..432
 BASE COUNT 77 a 139 c 149 g 67 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 |||||
 Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
 AR062056/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062056
 DEFINITION Sequence 135 from patent US 5843669.
 ACCESSION AR062056
 VERSION AR062056.1 GI:5989747
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 620)
 AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
 TITLE Cleavage of nucleic acid acid using thermostable methanococcus jannaschii FEN-1 endonucleases
 JOURNAL Patent: US 5843669-A 135 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..620
 BASE COUNT 103 a 202 c 214 g 101 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
 |||||
 Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
 AR062057/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062057
 DEFINITION Sequence 136 from patent US 5843669.
 ACCESSION AR062057
 VERSION AR062057.1 GI:5989748
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 620)
 AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
 TITLE Cleavage of nucleic acid acid using thermostable methanococcus

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:03 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20
Sequence: 1 tacgcgccttcgatgaccc 20

Scoring table: OLIGO_NTC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description

C	1	20	100.0	432	1	MSGRIFFRNAP	L05910 Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448 Sequence
C	3	20	100.0	620	6	AR062056	AR062056 Sequence
C	4	20	100.0	620	6	AR062057	AR062057 Sequence
C	5	20	100.0	620	6	AR062058	AR062058 Sequence
C	6	20	100.0	620	6	AR062059	AR062059 Sequence
C	7	20	100.0	620	6	AR062060	AR062060 Sequence
C	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AF060353	AF060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	I50706	I50706 Sequence 1
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MTU12205	MTU12205 Mycobacteri
C	14	20	100.0	5084	1	MSGRPOB	MSGRPOB Mycobacteri
C	15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
C	16	20	100.0	19770	1	MTC1376	MTC1376 Mycobacteri
C	17	17	85.0	3316	1	AF172323	AF172323 Bacillus
C	18	15	75.0	27	6	I50714	I50714 Sequence 9
C	19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
C	20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
C	21	15	75.0	239050	1	AL596169	AL596169 Listeria
C	22	14	70.0	143	3	AF277396	AF277396 Citrobact
C	23	14	70.0	409	1	CSPA622R	CSPA622R Agrobacte
C	24	14	70.0	442	8	AF080428	AF080428 Agrobacte
C	25	14	70.0	458	1	AF080421	AF080421 Agrobacte
C	26	14	70.0	518	1	AF325874	AF325874 Staphyloc
C	27	14	70.0	762	1	SHEPENC	SHEPENC S. flexneri
C	28	14	70.0	791	33	AC048639	AC048639 Giardia
C	29	14	70.0	1128	8	AB044172	AB044172 Yamagishi
C	30	14	70.0	1194	3	FHEFHMDA	FHEFHMDA Fasciola
C	31	14	70.0	1959	8	ATHTUBA6A	ATHTUBA6A Arabidopsi
C	32	14	70.0	2612	3	FHEFHMDR	FHEFHMDR Fasciola
C	33	14	70.0	2615	10	RNPKCEPA	RNPKCEPA R. norvegicu
C	34	14	70.0	3218	10	AF146518	AF146518 Rattus no
C	35	14	70.0	3240	8	SCU06465	SCU06465 Saccharomyc
C	36	14	70.0	3447	6	AR067447	AR067447 Sequence
C	37	14	70.0	3639	10	AF214568	AF214568 Rattus no
C	38	14	70.0	4075	10	AF146044	AF146044 Rattus no
C	39	14	70.0	4887	3	AY069181	AY069181 Drosophila
C	40	14	70.0	6211	3	CEFI1A5	CEFI1A5 Caenorhabdi
C	41	14	70.0	6275	6	AX345453	AX345453 Sequence
C	42	14	70.0	6275	6	AX348335	AX348335 Sequence
C	43	14	70.0	9086	1	AE001767	AE001767 Thermotog
C	44	14	70.0	9728	6	AX346805	AX346805 Sequence
C	45	14	70.0	9728	6	AX348479	AX348479 Sequence

ALIGNMENTS

RESULT 1
MSGRIFFRNAP/c 432 bp DNA linear BCT 21-MAY-1993
LOCUS Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 34(1), 647-650 (1993)
FEATURES
source
1..432
/organism="Mycobacterium tuberculosis"
/strain="H37"

JOURNAL Genome Res. 10 (12), 2030-2043 (2000)
 MEDLINE 20568492
 COMMENT On Aug 17, 1999 this sequence version replaced g1:5735350.

Contact: Brian Oliver
 Laboratory of Cellular and Developmental Biology
 NIDDK, National Institutes of Health
 6 Center Drive MSC 2715, Bldg 6, Rm BI-13, Bethesda, MD 20892 USA
 Fax: (301) 496 5239
 Email: oliverbhelix.nih.gov
<http://www.niddk.nih.gov/intram/people/boliver.htm>
 Tissue Isolation and Library construction performed at the National
 Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
<http://www.niddk.nih.gov/intram/people/boliver.htm>). DNA sequencing
 and analyses performed by National Institutes of Health Intramural
 Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
 Plate: 07 row: c column: 12
 Seq primer: M13R1 reverse primer (ABI).
 Location/Qualifiers

FEATURES
 source 1..379

/organism="Drosophila melanogaster"
 /strain="y[*] w[67c1]/Y"
 /db_xref="taxon:7227"
 /clone="ds07c12"
 /clone_lib="Drosophila melanogaster adult testis library"
 /sex="male"
 /dev_stage="1-5 day adult"
 /lab_host="SOLR (Stratagene)"
 /note="Organ: testis; Vector: pBluescript SK (Stratagene);
 Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
 day adult y[*] w[67c1]/Y males raised at 25°C. RNA
 isolated using Trizol (Life Technologies) and a single
 round of Poly(A)+ selection using oligotex (Qiagen). cDNA
 library constructed using Stratagene ZAP-cDNA synthesis
 kit. Oligo dT primed, size fractionated -1-6 kb, and
 directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
 Following a single round of amplification pBluescript SK
 phagemids were excised. A distribution channel for
 clones is being sought, but not currently available.
 Requests for clones cannot be honored."

BASE COUNT 104 a 96 c 113 g 66 t
 ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggtcggcgagctg 16
 ||||||||||||
 Db 39 ACGGTCGGCGAGCTG 53

Search completed: August 7, 2002, 23:12:33
 Job time: 11072 sec

RESULT 13
BE423869/c 237 bp mRNA linear EST 24-JUL-2000
LOCUS WHE0067_F05_K0925 wheat endosperm cDNA library Triticum aestivum
DEFINITION cDNA clone WHE0067_F05_K09, mRNA sequence.
ACCESSION BE423869
VERSION BE423869.1 GI:9421712
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 Triticeae; Triticum.
1 (bases 1 to 237)
Altenbach,S., Anderson,O.D., Chao,S., Gallil,G., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Endosperm cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strataene SK primer.
FEATURES
Source
1..237
Location/Qualifiers
/organism="Triticum aestivum"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0067_F05_K09"
/clone_lib="wheat endosperm cDNA library"
/issue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid: Site_1:
EcoRI; Seeds collected, endosperm isolated, and RNA
prepared by Susan Altenbach. Library constructed by
Strataene, Inc. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab."
BASE COUNT 65 a 79 c 40 g 53 t
ORIGIN
Query Match 75.0%; Score 15; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 tcgcgcagctatcc 20
|||||
Db 79 TCGCGAGCTGATCC 65
RESULT 14
A1945868 376 bp mRNA linear EST 08-JAN-2001
LOCUS bs17g07.y1 Drosophila melanogaster adult testis library Drosophila
DEFINITION melanogaster cDNA clone bs17g07 5', mRNA sequence.
ACCESSION A1945868
VERSION A1945868.2 GI:9991196
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 376)
Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and

TITLE
JOURNAL Gene discovery using computational and microarray analysis of
DEFINITION transcription in the drosophila melanogaster testis
MORLINE Genome Res. 10 (12), 2030-2043 (2000)
COMMENT 20568492
On Aug 17, 1999 this sequence version replaced gi:5736266.
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@helix.nih.gov,
http://www.niddd.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddd.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 17 row: 9 column: 07
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
Source
1..376
Location/Qualifiers
/organism="Drosophila melanogaster"
/strain="Y[*] w[67c1]/Y"
/db_xref="taxon:7227"
/clone="bs17g07"
/clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Strataene)"
/note="Organ: testis; Vector: pBluescript SK (Strataene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
day adult Y[*] w[67c1]/Y males raised at 25°C. RNA
isolated using Trizol (Life Technologies) and a single
round of poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Strataene ZAP-cDNA synthesis
kit. Oligo dt-primed, size fractionated -1.6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
BASE COUNT 110 a 94 c 107 g 65 t
ORIGIN
Query Match 75.0%; Score 15; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 acggtcgcgcagctg 16
|||||
Db 272 ACGGTCGCGAGCGTG 286
RESULT 15
A1944952 379 bp mRNA linear EST 08-JAN-2001
LOCUS bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
DEFINITION melanogaster cDNA clone bs07c12 5', mRNA sequence.
ACCESSION A1944952
VERSION A1944952.2 GI:9990300
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 379)
Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
Oliver,B.
Gene discovery using computational and microarray analysis of
transcription in the drosophila melanogaster testis

FEATURES

Location/Qualifiers
1. 606

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="533151"

/clone_lib="zebrafish adult brain"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

/lab_host="E. coli DH10B"

/note="Vector: pZiPlox; Site_1: NotI; Site_2: SalI;

Original library was constructed in lambdaZiPlox. Mass

excision of the cDNA library was performed to yield

pZiPlox plasmids. Insert check was done in original

library."

BASE COUNT

209 a 133 c 139 g 125 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 606;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcagctg 16

|||||

Db 452 TACGTCGCCGAGCTG 437

RESULT 11 640 bp mRNA linear EST 12-OCT-2001

BI888442 ZF637-2-000197 zebrafish shield stage whole embryo cDNA library

LOCUS MPMGP637 Danio rerio cDNA clone MPMGP637_18E17;MPMGP637E1718 5',

DEFINITION MRNA sequence.

ACCESSION BI888442.1 GI:16095713

VERSION EST.

KEYWORDS zebrafish.

SOURCE Danio rerio

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

; Cyprinidae; Danio.

1 (bases 1 to 640)

Clark,M., Amstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.

EST sequencing of a zebrafish shield stage cDNA library normalised

by oligonucleotide fingerprinting

Unpublished (2001)

JOURNAL

COMMENT

Contact: Hennig S

laboratory 123, dept. Lehrach

Max-Planck-Institut fuer Molekulare Genetik

Inhestr.63-73, D-14195 Berlin, Germany

Tel: +49 30 8413 1612

Fax: +49 30 8413 1360

Email: hennig@molgen.mpg.de

5' EST sequencing of clones from a zebrafish shield stage library,

normalised from 55,000 starting clones by oligonucleotide

fingerprinting

High quality sequence stop: 640.

Location/Qualifiers

1. 640

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="MPMGP637_18E17;MPMGP637E1718"

/clone_lib="zebrafish shield stage whole embryo cDNA

library MPMGP637"

/tissue_type="whole embryo"

/dev_stage="shield stage, 6 hrs post-fertilisation"

/lab_host="E.coli, XLI blue MRP"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;

oligo-dt-NotI primed, SalI adaptors, directionally cloned,

library normalised by oligonucleotide fingerprinting"

BASE COUNT

209 a 152 c 139 g 139 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 640;

Best Local Similarity 100.0%; Pred. No. 74;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcagctg 16

|||||

Db 541 TACGTCGCCGAGCTG 526

RESULT 12 708 bp mRNA linear EST 17-AUG-2000

BE585978 Est#7PT7_A09_a9_065 KSU wheat Fusarium graminearum infected spike

LOCUS cDNA library Triticum aestivum cDNA clone Est#7PT7_A09_a9_065, mRNA

DEFINITION sequence.

ACCESSION BE585978.1 GI:9839010

VERSION EST.

KEYWORDS bread wheat.

SOURCE Triticum aestivum

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae

; Triticeae; Triticum.

1 (bases 1 to 708)

Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.

The structure and function of the expressed portion of the wheat

genomes - Kansas State University. Fusarium graminearum infected

spike cDNA library

Unpublished (2000)

Contact: John Fellers

US Department of Agriculture, Agriculture Research Service, Plant

Science and Entomology Unit

Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State

University, Manhattan, KS 66506, USA

Tel: 785-532-2367

Fax: 785-532-6167

Email: jpf@falifa.ksu.edu

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20

Seq primer: 77.

Location/Qualifiers

1. 708

/organism="Triticum aestivum"

/cultivar="Suma13"

/db_xref="taxon:4565"

/clone="Est#7PT7_A09_a9_065"

/clone_lib="KSU wheat Fusarium graminearum infected spike

cDNA library"

/tissue_type="Spike"

/dev_stage="Adult Plant"

/lab_host="E. coli JM109"

/note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;

Plants were grown in the greenhouse. Spikes were sprayed

with Fusarium graminearum (at what stage). Total RNA, and

poly(A) RNA were prepared from infected spikes. cDNA was

prepared using the SmartTM PCR cDNA synthesis kit from

Clontech. cDNA was cloned into the pGEM-T easy vector

from Promega."

BASE COUNT 154 a 221 c 156 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 708;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gtccgcgcagctatcc 20

|||||

Db 559 GTCCGCGAGCTATCC 574

|||||

|||||

|||||

|||||

|||||

|||||

|||||

```

BASE COUNT      26 a      41 c      44 g      18 t      1 others
ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 130;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||||||
Db      90 gtcgcgcagctgattcc 75

RESULT 8
LOCUS    BM396091      132 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrachymena thermophila cDNA, mRNA sequence.
ACCESSION BM396091
VERSION   BM396091.1 GI:18196144
KEYWORDS EST.
SOURCE    Tetrachymena thermophila.
ORGANISM Tetrachymena thermophila.
REFERENCE Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
AUTHORS   'J. and Klobutcher, L.'
TITLE     EST from Tetrachymena thermophila, strain C0428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
           Molecular Genetics and Cell Biology
           University of Chicago
           920 E. 58th Street, Chicago, IL 60637, USA
           Tel: 773 702 4374
           Fax: 773 702 3172
           Email: apturkew@midway.uchicago.edu
           Seq primer: 73.

FEATURES
source    Location/Qualifiers
           1..132
           /organism="Tetrachymena thermophila"
           /strain="C0428.1"
           /db_xref="taxon:5911"
           /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
           /note="Vector: Bluescript2 SK+; Details on library
           preparation can be found in Chilcoat and Turkewitz (2001)
           Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      27 a      42 c      44 g      19 t

ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||||||
Db      92 gtcgcgcagctgattcc 77

RESULT 9
LOCUS    BM398255      134 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrachymena thermophila cDNA, mRNA sequence.
ACCESSION BM398255
VERSION   BM398255.1 GI:18196308
KEYWORDS EST.
SOURCE    Tetrachymena thermophila.
ORGANISM Tetrachymena thermophila.
REFERENCE Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
AUTHORS   'J. and Klobutcher, L.'
TITLE     EST from Tetrachymena thermophila, strain C0428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
           Molecular Genetics and Cell Biology
           University of Chicago
           920 E. 58th Street, Chicago, IL 60637, USA
           Tel: 773 702 4374
           Fax: 773 702 3172
           Email: apturkew@midway.uchicago.edu
           Seq primer: 73.

FEATURES
source    Location/Qualifiers
           1..134
           /organism="Tetrachymena thermophila"
           /strain="C0428.1"
           /db_xref="taxon:5911"
           /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
           /note="Vector: Bluescript2 SK+; Details on library
           preparation can be found in Chilcoat and Turkewitz (2001)
           Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      26 a      44 c      46 g      18 t

ORIGIN

```

```

REFERENCE 1 (bases 1 to 134)
AUTHORS   Turkewitz, A.P., Karer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
           'J. and Klobutcher, L.'
TITLE     EST from Tetrachymena thermophila, strain C0428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
           Molecular Genetics and Cell Biology
           University of Chicago
           920 E. 58th Street, Chicago, IL 60637, USA
           Tel: 773 702 4374
           Fax: 773 702 3172
           Email: apturkew@midway.uchicago.edu
           Seq primer: 73.

FEATURES
source    Location/Qualifiers
           1..134
           /organism="Tetrachymena thermophila"
           /strain="C0428.1"
           /db_xref="taxon:5911"
           /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
           /note="Vector: Bluescript2 SK+; Details on library
           preparation can be found in Chilcoat and Turkewitz (2001)
           Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      26 a      44 c      46 g      18 t

ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||||||
Db      94 gtcgcgcagctgattcc 79

RESULT 10
LOCUS    BI981973      606 bp      mRNA      linear      EST 24-OCT-2001
DEFINITION zebrafish adult brain Danio rerio cDNA clone 5333151 5'
           similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
ACCESSION BI981973
VERSION   BI981973.1 GI:16371108
KEYWORDS EST.
SOURCE    zebrafish.
ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 606)
AUTHORS   Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy
           'S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
           'K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
           Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritzer, E.,
           Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
           and Wilson, R.
TITLE     Washu zebrafish EST Project 1998
JOURNAL   Unpublished (1998)
COMMENT   Other-ESTs: fu53f08.x1
           Contact: Stephen L. Johnson
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: zbrafish@watson.wustl.edu
           CDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
           Matthew Clark. DNA Sequencing by: Washington University Genome
           Sequencing Center Clone Distribution: Genome Systems, St. Louis,
           Missouri (web address: www.genomesystems.com) (email contact:
           info@genomesystems.com) and Research Genetics, Huntsville, Alabama
           (web address: www.resgen.com) (email contact: info@resgen.com) and
           Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
           www.rzpd.de)
           High quality sequence stop: 446.

```

/tissue_type="root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="vector: lambda Uni-ZAP XR, excised phagemid
pbluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close Lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pbluescript phagemids before
normalization library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 144 a 209 c 165 g 140 t
ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgagctgattcc 20
|||||
Db 512 GGTGGCGAGCTGATCC 528

RESULT 6 828 bp mRNA linear EST 17-OCT-2001
LOCUS BG299722
DEFINITION HVSMEa0021120f Hordeum vulgare seedling shoot EST library
HVCNDA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
mRNA sequence.
BG299722
ACCESSION BG299722.1 GI:13087434
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Fritsch, D., Yu,
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
Fenton, R.D. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex cold-stressed seedling shoot cDNA
library
1 (bases 1 to 828)
Triticaceae; Hordeum.

JOURNAL
COMMENT
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 574
Seq primer: AATTAACTCCTCACTAAGGG
High quality sequence stop: 643.
Location/Qualifiers
1. 828

FEATURES
Source
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEa0021120f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCNDA0001 (Cold stress)"
/tissue_type="Seedling shoot"

/lab_host="TJCl21"
/note="vector: lambdaZAP, Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 50C for 2 days. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 600000 pfu
were in vivo excised to give pbluescript SK(-) cDNA
phagemids. These steps were performed in the TJ Close
laboratory at the University of California, Riverside
(Choi, Close, Fenton). Phagemids were plated and picked at
the Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Fritsch, Atkins and Wing). Plasmid DNA preparations
, DNA sequencing and sequence analysis were performed at
CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t
ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgagctgattcc 20
|||||
Db 500 GGTGGCGAGCTGATCC 516

RESULT 7 130 bp mRNA linear EST 17-JAN-2002
LOCUS BM397871/C
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM397871
ACCESSION BM397871.1 GI:18197924
VERSION
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila.
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 130)
Turkewitz A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. 130

FEATURES
Source
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and ceftaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the pT Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pluscript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcgcgcagctgattcc 20
|||||
Db 514 ggtcgcgcagctgattcc 530

RESULT 4
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEH0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0088E21f,
mRNA sequence.

ACCESSION BE195103
VERSION BE195103.3 GI:16321083
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 610)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton
R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.

JOURNAL Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 238
Seq primer: AATTAACCTCCTCACTAAGG
High quality sequence stop: 563.

FEATURES
Source
1..610
Location/Qualifiers

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,

30 and 45 DAP (Fenton). Total RNA was prepared from each pool. Equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluscript SK(-) cDNA phagemids (Choi) in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 127 a 203 c 158 g 120 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcgcgcagctgattcc 20
|||||
Db 499 ggtcgcgcagctgattcc 515

RESULT 5
LOCUS BE442518 658 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1101_H10_O19Zs wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA
sequence.

ACCESSION BE442518
VERSION BE442518.1 GI:9442034
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 658)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)

JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES
Source
1..658
Location/Qualifiers

/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
/clone_lib="wheat etiolated seedling root normalized cDNA
library"

/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gtcgcgcagctgattcc 20
|||||
Db 86 gtcgcgcagctgattcc 102

RESULT 2
BE445100 544 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_H08_P16ZS wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
sequence.
ACCESSION BE445100 GI:9444655
VERSION BE445100.1
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
AUTHORS 1 (bases 1 to 544)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_1lb="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the T7 Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gtcgcgcagctgattcc 20
|||||
Db 512 gtcgcgcagctgattcc 528

RESULT 3
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1137_H03_005ZS wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713 GI:9444264
VERSION BE444713
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae
AUTHORS 1 (bases 1 to 558)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_1lb="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:33 : Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20

Sequence: 1 tacggtcgcgcgcgcgcgc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST.*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estcpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_lin:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	85.0	422	10	BE443802 WHE1122.B
2	17	85.0	544	10	BE445100 WHE1132.H
3	17	85.0	558	10	BE444713 WHE1137.H
4	17	85.0	610	9	BE195103 HVSMEH008
5	17	85.0	658	10	BE442518 WHE1101.H
6	17	85.0	828	10	BG299722 HVSME002
7	16	80.0	130	10	BM397871 5009-0-38
8	16	80.0	132	10	BM396091 5009-0-17
9	16	80.0	134	10	BM398255 5009-0-42
10	16	80.0	606	10	BI981973 fUS3108.Y
11	16	80.0	640	10	BI888442 ZF637-2-0
12	16	80.0	708	10	BE585978 Est#7PT7
13	15	75.0	237	10	BE423869 WHE0067.F
14	15	75.0	376	9	AI945868 bs17907.Y
15	15	75.0	379	9	AI944952 bs07c12.Y
16	15	75.0	556	12	BH229591 1006153CO
17	15	75.0	568	10	BI628597 RH57079.5

18	15	75.0	652	10	BF489438
19	15	75.0	655	10	BF489430
20	15	75.0	667	10	BF489536
21	15	75.0	703	10	BF496035
22	15	75.0	722	10	BF496005
23	15	75.0	958	10	BE969326
24	15	75.0	984	12	CNS01GJ2
25	15	75.0	1000	10	BG416363
26	15	75.0	1188	10	BM477266
27	14	70.0	159	10	BI727507
28	14	70.0	180	10	C61884
29	14	70.0	239	10	BF920601
30	14	70.0	251	12	AQ096217
31	14	70.0	252	10	W87730
32	14	70.0	292	9	BB347857
33	14	70.0	299	10	BI133481
34	14	70.0	318	10	M79472
35	14	70.0	328	9	AM922029
36	14	70.0	329	10	H57342
37	14	70.0	339	9	AJ281216
38	14	70.0	344	10	BE415176
39	14	70.0	349	9	AU110574
40	14	70.0	349	10	BG274757
41	14	70.0	352	10	T83696
42	14	70.0	360	9	AV186178
43	14	70.0	360	9	AV191317
44	14	70.0	360	9	AV192208
45	14	70.0	360	9	AV197881

ALIGNMENTS

RESULT 1
LOCUS BE443802 422 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1122.B06.C122S Wheat etiolated seedling root normalized CDNA library Triticum aestivum cdna clone WHE1122.B06.C12, mRNA sequence.
ACCESSION BE443802
KEYWORDS BE443802.1 GI:9443341
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 422)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C., and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized root cdna library
Unpublished (2000)
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratiagene SK primer.
Location/Qualifiers
1..422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122.B06.C12"
/clone_lib="Wheat etiolated seedling root normalized CDNA library"
/tissue_type="Root"

This Page Blank (uspto)


```
FT primer_bind /note="primer rpo397"
FT primer_bind 952..966
FT primer_bind /*tag= s
FT primer_bind /note="primer NMORO-1"
FT primer_bind 952..966
FT primer_bind /*tag= t
FT primer_bind /note="primer NMORO-2"
XX
XX WO9533074-A1.
XX
XX 07-DEC-1995.
XX
XX 26-MAY-1995: 95MO-US06790.
XX
XX 26-MAY-1994: 94US-0250030.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Fellmeier TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX Young KK;
XX
XX WPI: 1996-030581/03.
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Disclosure: Fig. 3; 54pp: English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The 1st several bases comprise a
XX nonhybridizing tail consisting of filler bases followed by
XX a restriction site incorporated to facilitate cloning using the
XX amplicon at a later date, if desired. The remaining bases hybridize
XX to bacterial rpoB DNA. The method provides for the detection of M.
XX tuberculosis and the concurrent determination of its drug
XX susceptibility, particularly to rifampin. The method can provide
XX often greater than 95% sensitivity and 100% specificity. The
XX biological sample is a fluid or tissue sample from a human.
XX
XX Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 17; Length 970;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 tacggtcgagcgtcatcc 20
XX ||||||||||||||||
XX Db 261 tacggtcgagcgtcatcc 280
XX
XX RESULT 15
XX AAH51976
XX ID AAH51976 standard; DNA: 3519 BP.
XX
XX AC AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000MO-US31152.
XX
```

```
PR 12-NOV-1999: 99US-0165086.
PR 12-NOV-1999: 99US-0165124.
PR 01-FEB-2000: 2000US-0179531.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI: 2001-329193/34.
XX P-PSDB: AAG81125.
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
XX involves providing algorithm that analyzes a functional relationship
XX between nucleotide or polypeptide sequences, and comparing the
XX sequences
XX
XX Disclosure: Page 68-69; 207pp: English.
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX algorithm capable of analysing a functional relationship between
XX nucleotide and polypeptide sequences. The method is useful for
XX characterising the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3519;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 tacggtcgagcgtcatcc 20
XX ||||||||||||||||
XX Db 1119 tacggtcgagcgtcatcc 1138
XX
```

Search completed: August 8, 2002, 00:01:25
Job time: 7614 sec

```
Db      18  tacgtcgcgcagctgatcc 37
|||||
RESULT 13
AAAA9863
ID      AAAA9863 standard; DNA: 480 BP.
XX
XX      AAAA9863;
AC
XX      25-SEP-2000 (first entry)
DT
XX      Mycobacterium tuberculosis rpoB gene (rifampin resistance).
DE
XX      Antibiotic resistance: rpoB gene: rifampin resistance; ss.
XX      Mycobacterium tuberculosis.
OS
XX      Key
FH      Location/Qualifiers
FT      primer_bind
FT      complement(41..60)
FT      /tag= a
FT      /note= "primer of AAAA9823"
FT      primer_bind
FT      372..391
FT      /tag= b
FT      /note= "primer of AAAA9824"
XX
XX      WO200036142-A1.
XX
XX      22-JUN-2000.
XX
XX      10-DEC-1999; 99WO-CA01177.
XX
XX      11-DEC-1998; 98US-0111794.
XX
XX      (VISI-) VISIBLE GENETICS INC.
XX
XX      Shipman R;
XX
XX      WPI; 2000-431611/37.
XX
XX      Method for the detection and characterization of Mycobacterium
XX      tuberculosis with antibiotic resistance in a sample -
XX
XX      Disclosure: Page 5; 43pp; English.
XX
XX      The present sequence is that of the Mycobacterium tuberculosis
XX      rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
XX      cycle sequencing primers (see AAA49823-62) are used for the detection
XX      and analysis of antibiotic resistance-associated mutations in
XX      defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
XX      (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
XX      (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
XX      (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
XX      These primers can be used in a method for the detection and
XX      characterization of M. tuberculosis present in a sputum sample.
XX      The method involves performing a sequencing procedure, with or
XX      without prior amplification, to detect the presence of M.
XX      tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
XX      and 23S genes for the presence of antibiotic-inducing mutations.
XX      If M. tuberculosis is detected, a second sequencing procedure is
XX      performed on the sample to evaluate additional genes for the
XX      presence of antibiotic resistance-inducing mutations. Genotypic
XX      tests are rapid, sensitive and accurate providing information as to
XX      antibiotic treatment options.
XX
XX      Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other:
SQ
Query Match      100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  tacgtcgcgcagctgatcc 20
```

```
Db      41  tacgtcgcgcagctgatcc 60
|||||
RESULT 14
AAT09676
ID      AAT09676 standard; DNA: 970 BP.
XX
XX      AAT09676;
AC
XX      15-OCT-1996 (first entry)
DT
XX      Mycobacterium tuberculosis rpoB gene DNA sequence.
DE
XX      Tuberculosis; disease diagnosis: oligonucleotide: DNA primer; PCR;
XX      polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX      Mycobacterium tuberculosis.
OS
XX      Key
FH      Location/Qualifiers
FT      primer_bind
FT      10..27
FT      /tag= a
FT      /note= "primer FENLFF"
FT      primer_bind
FT      226..243
FT      /tag= b
FT      /note= "primer DDIDHL"
FT      primer_bind
FT      226..240
FT      /tag= c
FT      /note= "primer DDIDH"
FT      primer_bind
FT      338..364
FT      /tag= d
FT      /note= "primer rpo95"
FT      primer_bind
FT      348..373
FT      /tag= e
FT      /note= "primer rpo105"
FT      primer_bind
FT      354..373
FT      /tag= f
FT      /note= "primer KY290"
FT      misc_feature
FT      372..373
FT      /tag= g
FT      /note= "M. tuberculosis signature nucleotide"
FT      433..434
FT      /tag= h
FT      /note= "M. tuberculosis signature nucleotide"
FT      438
FT      /tag= i
FT      /note= "M. tuberculosis signature nucleotide"
FT      468..469
FT      /tag= j
FT      /note= "M. tuberculosis signature nucleotide"
FT      486
FT      /tag= k
FT      /note= "M. tuberculosis signature nucleotide"
FT      501
FT      /tag= l
FT      /note= "M. tuberculosis signature nucleotide"
FT      516
FT      /tag= m
FT      /note= "M. tuberculosis signature nucleotide"
FT      516..535
FT      /tag= n
FT      /note= "primer rpo273"
FT      misc_feature
FT      525
FT      /tag= o
FT      /note= "M. tuberculosis signature nucleotide"
FT      525..541
FT      /tag= p
FT      /note= "primer KY292"
FT      primer_bind
FT      536..562
FT      /tag= q
FT      /note= "primer rpo293"
FT      primer_bind
FT      640..666
FT      /tag= r
```


DR WPI; 2002-075472/10.
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
PS Disclosure; Page 21; 74pp; English.
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcgagctgacc 20
|||||
DB 5 tacggtcgcgcgagctgacc 24
RESULT 9
AAS99527 100.0%; Score 20; DB 24; Length 306;
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
OS
PN WO200192573-A1.
PN
PD 06-DEC-2001.
PD
PF 30-MAY-2001; 2001WO-KR00904.
PF
PR 30-MAY-2000; 2000KR-0029369.
PR
PA (BIOM-) BIOMEDLAB CO LTD.
PA
PI Kim H, Kim N, Yoon S, Kim J, Park M;
PI
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
PS Disclosure; Page 21; 74pp; English.

XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcgagctgacc 20
|||||
DB 5 tacggtcgcgcgagctgacc 24
RESULT 10
AAS99530 100.0%; Score 20; DB 24; Length 306;
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
OS
PN WO200192573-A1.
PN
PD 06-DEC-2001.
PD
PF 30-MAY-2001; 2001WO-KR00904.
PF
PR 30-MAY-2000; 2000KR-0029369.
PR
PA (BIOM-) BIOMEDLAB CO LTD.
PA
PI Kim H, Kim N, Yoon S, Kim J, Park M;
PI
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
PS Disclosure; Page 21; 74pp; English.
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of


```
ID AAX27179 standard; DNA: 306 BP.
XX
XX AAX27179;
AC
XX 27-MAY-1999 (first entry)
DT
XX
XX RpoB gene fragment.
DE
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria bovis.
OS
XX
XX MO9905316-A1.
PN
XX 04-FEB-1999.
PD
XX
XX 28-JUL-1998; 98KR-0000228.
PF
XX
XX 28-JUL-1997; 97KR-0035501.
PR
XX
XX (BION-) BIONEER CORP.
PA
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
DR
XX
XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PS species, useful for detecting and identifying mycobacterial species
XX
XX Claim 8; Page 64; 91pp; English.
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgcgcgagctgaccc 20
    |||||||
DB 5 tacggtcgcgcgagctgaccc 24
RESULT 7
AAX27180
ID AAX27180 standard; DNA: 306 BP.
XX
XX AAX27180;
AC
XX
XX 27-MAY-1999 (first entry)
DT
XX
XX RpoB gene fragment.
DE
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria bovis.
OS
```

```
PN MO9905316-A1.
XX
XX 04-FEB-1999.
PD
XX
XX 28-JUL-1998; 98KR-0000228.
PF
XX
XX 28-JUL-1997; 97KR-0035501.
PR
XX
XX (BION-) BIONEER CORP.
PA
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
DR
XX
XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PS species, useful for detecting and identifying mycobacterial species
XX
XX Claim 9; Page 64; 91pp; English.
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgcgcgagctgaccc 20
    |||||||
DB 5 tacggtcgcgcgagctgaccc 24
RESULT 8
AAS99526
ID AAS99526 standard; DNA: 306 BP.
XX
XX AAS99526;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Mycobacterium species identification primer #1.
DE
XX
XX Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO200192573-A1.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 30-MAY-2001; 2001WO-KR00904.
PF
XX
XX 30-MAY-2000; 2000KR-0029369.
PR
XX
XX (BION-) BIOMEDLAB CO LTD.
PA
XX
XX Kim H, Kim N, Yoon S, Kim J, Park M;
PI
XX
```

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpoB*, *kacB*, *rpsL*/*sls2*
CC and *23S* genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 1 tacgctcgagcagctgattcc 20

RESULT 4

AAx27214
ID AAX27214 standard; DNA; 306 BP.

AC AAX27214;

DT 27-MAY-1999 (first entry)

DE *rpoB* gene fragment.

XX *rpoB* gene: mycobacteria; phylogenetic tree construction;

KW mycobacterial species identification; phylogenetic analysis; ss.

XX Mycobacteria tuberculosis.

OS WO9905316-A1.

XX 04-FEB-1999.

PD 28-JUL-1998; 98KR-0000228.

PF 28-JUL-1997; 97KR-0035501.

PR 28-JUL-1997; 97KR-0035501.

XX (BION-) BIONEER CORP.

XX Kim B, Kook Y;

PI WPI; 1998-539367/46.

DR New pair of polymerase chain reaction (PCR) primers - for

PT sequence-specific amplification of the *rpoB* gene from mycobacterial

PS species, useful for detecting and identifying mycobacterial species

XX Claim 43; Page 75-76; 91pp; English.

CC This sequence represents a mycobacterial *rpoB* gene fragment, that is

CC amplified using the PCR primers of the invention. The primers form a

CC method of detecting and identifying mycobacterial species by constructing

CC a phylogenetic tree for the species. The use of the primers for

CC sequence-specific amplification of the *rpoB* gene (encoding the beta

CC subunit of RNA polymerase) from mycobacterial species provides an

CC efficient way of characterising these species. In addition to

CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to

CC the 16S rRNA gene because it has four subunits, which are highly

CC conserved throughout prokaryotes. The method is particularly useful for

CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin

CC susceptibility can be simultaneously determined in *M. tuberculosis*.

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 5 tacgctcgagcagctgattcc 24

RESULT 5

AAx27175
ID AAX27175 standard; DNA; 306 BP.

AC AAX27175;

DT 27-MAY-1999 (first entry)

DE *rpoB* gene fragment.

XX *rpoB* gene: mycobacteria; phylogenetic tree construction;

KW mycobacterial species identification; phylogenetic analysis; ss.

XX Mycobacteria africanum.

OS WO9905316-A1.

XX 04-FEB-1999.

PD 28-JUL-1998; 98KR-0000228.

PF 28-JUL-1997; 97KR-0035501.

PR 28-JUL-1997; 97KR-0035501.

XX (BION-) BIONEER CORP.

XX Kim B, Kook Y;

PI WPI; 1998-539367/46.

DR New pair of polymerase chain reaction (PCR) primers - for

PT sequence-specific amplification of the *rpoB* gene from mycobacterial

PS species, useful for detecting and identifying mycobacterial species

XX Claim 4; Page 62-63; 91pp; English.

CC This sequence represents a mycobacterial *rpoB* gene fragment, that is

CC amplified using the PCR primers of the invention. The primers form a

CC method of detecting and identifying mycobacterial species by constructing

CC a phylogenetic tree for the species. The use of the primers for

CC sequence-specific amplification of the *rpoB* gene (encoding the beta

CC subunit of RNA polymerase) from mycobacterial species provides an

CC efficient way of characterising these species. In addition to

CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to

CC the 16S rRNA gene because it has four subunits, which are highly

CC conserved throughout prokaryotes. The method is particularly useful for

CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin

CC susceptibility can be simultaneously determined in *M. tuberculosis*.

XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 5 tacgctcgagcagctgattcc 24

RESULT 6

AAx27179

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. lepreae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcgagctgattcc 20
Db 1 tacggtcgcgcgagctgattcc 20
|||||
RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823:
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
XX ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcgagctgattcc 20
Db 1 tacggtcgcgcgagctgattcc 20
|||||
RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825:
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
XX ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826
CC and with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:22 : Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20
Sequence: 1 tacggtcgcgcagctgattcc 20

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 1736436 segs, 858457221 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: N.Geneseq_032802:*

```
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	17	AA12092
2	20	100.0	20	21	AAA49823
3	20	100.0	20	21	AAA49825
4	20	100.0	306	19	AAx27214
5	20	100.0	306	19	AAx27175
6	20	100.0	306	19	AAx27179
7	20	100.0	306	19	AAx27180
8	20	100.0	306	24	AAx27180
9	20	100.0	306	24	AAx27180

10	20	100.0	306	24	AAx27180	Mycobacterium spec
11	20	100.0	306	24	AAx27180	Mycobacterium spec
12	20	100.0	432	14	AAx27180	Mycobacterium spec
13	20	100.0	480	21	AAx27180	Mycobacterium spec
14	20	100.0	970	17	AAx27180	Mycobacterium spec
15	20	100.0	3519	22	AAx27180	Mycobacterium spec
16	20	100.0	3534	22	AAx27180	Mycobacterium spec
17	20	100.0	3853	21	AAx27180	Mycobacterium spec
18	20	100.0	3853	21	AAx27180	Mycobacterium spec
19	19	95.0	306	24	AAx27180	Mycobacterium spec
20	19	95.0	306	24	AAx27180	Mycobacterium spec
21	19	95.0	21500	23	AAx27180	Mycobacterium spec
22	18	90.0	25	17	AAx27180	Mycobacterium spec
23	18	90.0	87	22	AAx27180	Mycobacterium spec
24	16	80.0	306	19	AAx27180	Mycobacterium spec
25	16	80.0	306	19	AAx27180	Mycobacterium spec
26	16	80.0	306	19	AAx27180	Mycobacterium spec
27	16	80.0	306	19	AAx27180	Mycobacterium spec
28	16	80.0	306	19	AAx27180	Mycobacterium spec
29	16	80.0	306	19	AAx27180	Mycobacterium spec
30	16	80.0	306	19	AAx27180	Mycobacterium spec
31	16	80.0	306	19	AAx27180	Mycobacterium spec
32	16	80.0	306	19	AAx27180	Mycobacterium spec
33	16	80.0	306	19	AAx27180	Mycobacterium spec
34	16	80.0	306	19	AAx27180	Mycobacterium spec
35	16	80.0	306	19	AAx27180	Mycobacterium spec
36	16	80.0	306	19	AAx27180	Mycobacterium spec
37	16	80.0	306	19	AAx27180	Mycobacterium spec
38	16	80.0	306	19	AAx27180	Mycobacterium spec
39	15	75.0	27426	23	AAx27180	Mycobacterium spec
40	15	75.0	2488	23	AAx27180	Mycobacterium spec
41	15	75.0	2772	23	AAx27180	Mycobacterium spec
42	15	75.0	4544	23	AAx27180	Mycobacterium spec
43	15	75.0	4403765	22	AAx27180	Mycobacterium spec
44	15	75.0	4411529	22	AAx27180	Mycobacterium spec
45	14	70.0	50	19	AAx27180	Mycobacterium spec

ALIGNMENTS

RESULT 1	
AA12092	AA12092 standard; DNA: 20 BP.
ID	AA12092
XX	AA12092
AC	AA12092
XX	AA12092
DT	10-JUL-1996 (first entry)
XX	
DE	M. tuberculosis rpoB gene fragment amplification primer p2.
XX	
KW	Antibiotic resistance; spectrum; gene; mycobacterium;
KW	determination; amplification; tuberculosis; rpoB; fragment;
KW	primer; differential; hybridisation; pattern; rifampicin;
KW	rifabutin; species identification; ss.
XX	
OS	Synthetic.
XX	
PN	W09533851-A2.
PD	14-DEC-1995.
XX	
PF	09-JUN-1995; 95WO-EF02230.
XX	
PR	09-JUN-1994; 94EP-0870093.
XX	
PI	(INNO-) INNOGENETICS NV.
XX	
PI	De Beenhouwer H, Jannes G, Machielinckx L, Portels F;
XX	Rosau R;
DR	WPI; 1996-040250/04.
XX	

This Page Blank (uspto)

ORGANISM
Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 3534)
Bergerson, M.G., Bolshtynova, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL
Patent: WO 0123604-A 2002-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source
1. 3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT
679 a 1081 c 1188 g 586 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 3.1; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
QY 1 tacggtcggcagctgaccc 20
|||||
Db 1137 TACGTCGCGAGCTGATCC 1156
RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS
Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION
gene, partial cds.
VERSION
U12205
KEYWORDS
U12205.1 GI:515684
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkhardt, T.
TITLE
The rpoB gene of Mycobacterium tuberculosis
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 3853)
Imboden, P.
TITLE
Direct Submision
AUTHORS
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
JOURNAL
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
FEATURES
source
1. 3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576. >3853
/gene="rpoB"
576. >3853
/gene="rpoB"
/codon_start=1
/transl_table=11
/product="RNA-polymerase beta subunit"
/protein_id="AA02042.2"
/db_xref="GI:714449"
/translation="MLECCILADSRQSKTAASPSRPOSSNNNSVPGAPNRYVPAKL
REPLEPGLIVQTSFEMILGSPMRSAERAGVNPVGLAEVLELSPIDEDSGS
MSLSPSRPDVQAPVDECKDKMTVAAPLEVTAFINNNNGEIKSOTVEMGDEPDM
TEKGTFTINGTERRVVSOLVRSRGVYFDETDKSLDKLHSAKVIKPSGAMLEPVDK
RDTVGVRIDRRRQPVTLKALGWTSSQIVERRGSEIMRSTLEKDNVTGIDELLD
IYRKLRPGEPTKESAOPLLENLFPKERRYDLARGRYKVNKILGLHVGEPITSTLT

EEDVATIEYLVRLHGCOTTMVPGVEVPEVETDIDHRCNRRRLTVGCLIONOIRVG
MSMERVRRERMTTQDVEAITPQTLINIRVVAALKEFGTSLQSPMDONNELSLT
HKRRLSALGGGLSRERAGLEVDPVPSHYGRMCPIETEGPNIGLISLSYARVNP
FGIETPYRKVVDGVSDGIYVLTADDEDRHVAQANSPIDAGREVRVLRKAGP
EVEYVPSSEVDVDSPPROMSVATAMIPLEHDDNRALMGANMORAVPLVRSAP
LVCTGHELRALIDATSSSGECSGTEEVASDYITVHNDGTRRTYMRKFRANSNGTC
ANOCPIVDAGDRVDAQVINDGCTDDEGEMALKNLIVAIMPEGHNYEDATILSNRL
VEEDVLTSLHIEHEIDAROTKGAEEITRDIPNISDEVLAIDLDERGIVRIGAEVNDG
DILVGVTPKGETELTPEERILRAIFGEKAREVDSLSKVPHEGSKVIGIRVFSRD
EDELPAVGNELVAVYVAOKRKISDGLAGRHGKNGVIGKILPVEDMPFLADPTVDI
ILNTHGVPRRMTIGOLLETHLGCAHSGKRVDAKGVPMARLPPDELEACPNAIVS
TVPFDGAQEALEOGLSCTIPNRDGVYINDGKAMLPDGRSGEPPPYPTVGYNYIM
KLHLVDDKIHARSTGPTSMITQOPLGKAKQFGCGRGENEHCNAMAQAYGAAVYLOELL
TIKS"
BASE COUNT
723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 3; Mismatches 0; Gaps 0;
Matches 20; Conservative 0; Indels 0; Gaps 0;
QY 1 tacggtcggcagctgaccc 20
|||||
Db 1712 TACGTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 23:49:03
Job time: 9217 sec

	FEATURES	Location/Qualifiers
source	1..432	/organism="Mycobacterium tuberculosis"
		/strain="H37"
		/db_xref="taxon:1773"
CDS	<1..>.432	
	/codon_start=1	
	/transl_table=11	
	/product="RNA polymerase beta subunit"	
	/protein_id="AAB59068.1"	
	/db_xref="GI:149992"	
	/translation="GNRRRTVGGELIONIRGSMRERVREMTVDVAITPRTI INIRYVAIKEFETSOLOMDONNPLSGTHRRLSALGPGLSERAGLEVRYD HSHRGMRCPITPEPGPNLIGSLSYARNPGEFTPYR"	
variation	149	/phenotype="rifampicin resistant in association with mutation 234 G" replace="c"
variation	188	/phenotype="rifampicin resistant" replace="c"
variation	191	/phenotype="rifampicin resistant" replace="c"
variation	194	/phenotype="rifampicin resistant in association with mutation 203 T" replace="c"
variation	203	/phenotype="rifampicin resistant" replace="t"
variation	208..210	/phenotype="rifampicin resistant" replace="t"
variation	232	/phenotype="rifampicin resistant" replace="" phenotype="rifampicin resistant"
variation	232	/phenotype="rifampicin resistant" replace="g"
variation	233	/phenotype="rifampicin resistant" replace="a"
variation	233	/phenotype="rifampicin resistant" replace="g"
variation	234	/phenotype="rifampicin resistant" replace="c"
variation	247..248	/phenotype="rifampicin resistant" replace="g"
variation	248	/phenotype="rifampicin resistant" replace="ca"
variation	248	/phenotype="rifampicin resistant" replace="g"
variation	254	/phenotype="rifampicin resistant" replace="t"
variation	254	/phenotype="rifampicin resistant" replace="c"
BASE COUNT	77 a 140 c 148 g 67 t	
ORIGIN		
Query Match	100.0%	Score 20; DB 1; Length 432;
Best Local Similarity	100.0%;	Pred. No. 4,3;
Matches 20; Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
DB	18 TACGCTCGCAGCATGATCC 37	
OY	1 tacgctcgagcgcgatcc 20	

RESULT	12				
LOCUS	AR067448				
DEFINITION	AR067448	432 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	Sequence 59 from patent US 5851763.				
VERSION	AR067448				
KEYWORDS	AR067448.1	GI:5998670			
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 432)				
	Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and Bodmer, J.				
TITLE	Rapid detection of antibiotic resistance in mycobacterium tuberculosis				
JOURNAL	Patent: US 5851763-A 59 22-DEC-1998;				
FEATURES	Location/Qualifiers				
source	1..432				
	/organism="unknown"				
BASE COUNT	77 a 139 c 149 g 67 t				
ORIGIN					

Query Match	100.0%	Score 20;	DB 6;	length 432;
Best Local Similarity	100.0%	Pred. NC 4.3;		
Matches	20;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	1	tacgctgcgcagctgatcc	20
Db	18	TACGGTCGGCGAGCTGATCC	37

RESULT 13

LOCUS	I50706	970 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 1 from patent US 5643723.				
ACCESSION	I50706				
VERSION	I50706.1	GI:2472409			
KEYWORDS					
SOURCE	Unknown.				

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
Unclassified. 1 (bases 1 to 970)	Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.	Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens		Patent: US 5643723-A 1 01-JUL-1997;	Location/Qualifiers 1..970

BASE COUNT	182 a	302 c	330 g	156 t
ORIGIN	/organism="unknown"			

Query Match	100.0%	Score 20;	DB 6;	Length 970;
Best Local Similarity	100.0%	Pred. No. 3.8;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1  tacgctcgcgagctgattcc 20
          |||||
Db      261 TACGGTCGGCGAGCTGATCC 281

```

RESULT	14
AX111339	
LOCUS	
AX111339	3534 bp DNA
DEFINITION	Sequence 2072 from Patent WO0123604.
ACCESSION	AX111339
VERSION	AX111339.1 GI:13927631
KEYWORDS	
SOURCE	Mycobacterium tuberculosis.
	linear PAT 30-APR-2001

Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y.-H. and Kim,B.-J.
METHOD for identifying mycobacterial species by comparative
TITLE
Sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source 1..306
Location/Qualifiers
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgctatcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 8
LOCUS ARI57008 306 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
METHOD for identifying mycobacterial species by comparative
TITLE
Sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
source 1..306
Location/Qualifiers
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgctatcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 9
LOCUS ARI57042 306 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
METHOD for identifying mycobacterial species by comparative
TITLE
Sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
source 1..306
Location/Qualifiers
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgctatcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 10
LOCUS ARI57051 306 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
METHOD for identifying mycobacterial species by comparative
TITLE
Sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
source 1..306
Location/Qualifiers
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgctatcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA Linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
Mycobacterium tuberculosis (strain H37) DNA.
Mycobacterium tuberculosis
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 432)
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

```

Db      5  TACGGTCGGCAGCTGATCC 24

RESULT  4
LOCUS   AF057453
DEFINITION Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057453
VERSION   AF057453.1
KEYWORDS GI:5902493
SOURCE   Mycobacterium bovis BCG.
ORGANISM Mycobacterium bovis BCG.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y., and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE Direct Submission
JOURNAL Submitted (06-Apr-1998) Microbiology, Seoul National University College of Medicine, 28 Youn-gu, Chongno-gu, Seoul 110-799, Korea

FEATURES
source      1..306
             /organism="Mycobacterium bovis BCG"
             /strain="Tokyo 1172"
             /db_xref="taxon:33892"
             <1..>306
             /gene="rpoB"
             <1..>306
             /gene="rpoB"
             /codon_start=3
             /transl_table=11
             /product="RNA polymerase beta"
             /protein_id="AAD5517.1"
             /db_xref="GI:5902494"
             /translation="RTVGEILQNIIRVGSMSMERVREMTODVEAITPOTLINIRP
             VVAAIKEFGTSOLSCFMDQNNPLSGILTHRRRLSALGPGLSRRAGLEVRDHPHSH"

BASE COUNT 56 a 95 c 108 g 47 t

Query Match      100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcagctgatcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT  5
LOCUS   AF057454
DEFINITION Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057454
VERSION   AF057454.1
KEYWORDS GI:5902495
SOURCE   Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 2 05-JUN-2001;
FEATURES source      1..306
             /organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

Query Match      100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcagctgatcc 20
|||||

```

```

REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y., and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE Direct Submission
JOURNAL Submitted (06-Apr-1998) Microbiology, Seoul National University College of Medicine, 28 Youn-gu, Chongno-gu, Seoul 110-799, Korea

FEATURES
source      1..306
             /organism="Mycobacterium tuberculosis"
             /strain="H37Rv: ATCC27294"
             /db_xref="ATCC:27294"
             /db_xref="taxon:1773"
             <1..>306
             /gene="rpoB"
             <1..>306
             /gene="rpoB"
             /codon_start=3
             /transl_table=11
             /product="RNA polymerase beta"
             /protein_id="AAD5518.1"
             /db_xref="GI:5902496"
             /translation="RTVGEILQNIIRVGSMSMERVREMTODVEAITPOTLINIRP
             VVAAIKEFGTSOLSCFMDQNNPLSGILTHRRRLSALGPGLSRRAGLEVRDHPHSH"

BASE COUNT 56 a 95 c 108 g 47 t

Query Match      100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcagctgatcc 20
|||||
Db 5 TACGGTCGGCAGCTGATCC 24

RESULT  6
LOCUS   AR157003
DEFINITION Sequence 2 from patent US 6242584.
ACCESSION AR157003
VERSION   AR157003.1
KEYWORDS GI:15125707
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 2 05-JUN-2001;
FEATURES source      1..306
             /organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

Query Match      100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcagctgatcc 20
|||||

```


/product="AP endonuclease, family 2"
/protein_id="AAK44924.1"
/db_xref="GI:13880221"
/translation="MIGSHVSPDPPLAAAEAGADVQIFIGNQSKAKPKPRDAA
AKATLPIYVAPYLINLASANKRRLPSKRLIQCETCAADICAAYIVHGAVAD
DNDIKGFQWRKALDRLETEVYVLENTAGDQAMARFETIARLMVIGDTGFC
LDTCHTMAGELTDAVDRIKAITGRIDLVHNDNDESGSRDRHNLMSQIDPDL
LVAAYKAGAPVICTADGCRKDDIAFLERTGS"
10957. .11799
/gene="MT0700"
10957. .11799
/note="similar to GB:U00012 PID:466863; identified by
sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="hydrolase/esterase, putative"
/protein_id="AAK44925.1"
/db_xref="GI:13880222"
/translation="MLRRVAILLAVALAFAGCGSGTRLAAGFGNGSVHTLDVDGAG
SYRLKPYGLPSSAPLYVMLHGGFSGAKOERSYGMDELADSEKFLVAYPDGYHRAN
ANGGCGRPAREPAGDDIGFVRAVADIANNVSDPARVYTGMSNGAIMSTTLANT
STFRAIGVSGQLDPCOSPRPVYIHGTDPLVRYHGGPAGAFARIDGPVPFDLN
AFWRVNRGALDITTEGPTTSGATCADNRRVLLTVDAGHRWPSFATQTLWRFPA
AHFR"
11859. .13487
/gene="MT0701"
11859. .13487
/note="similar to SP:P33224 GB:U20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
putative"
/codon_start=1
/transl_table=1
/product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK44926.1"
/db_xref="GI:13880223"
/translation="MSDTHVYVNVPPLENYNPASSPYLIALIQEGOMGLDEVNEY
GAISASCOQRKMGELADNRNPILHTHDAYGYRDEVEYDPAYHELMRTAITHGMHAAP
WADRPGAHVRAKTSYVTEPGHICISMTYAVPALRYNSSELAVYEPILTSREY
DPELKPATTKAGITAGMSMTEKOGSDVRACTQATPRADSGYSLTGKKTSAWCD
ITVLAQAPDGLSCFLPRVLPDGTNRNRFLORLDKLGNHANSSEVEYDGAVALWV
GEBRGVPTITEMVNLTRLDCAIGSATSMRTGLTRAHHQAHRKAFGAYLIDQLMRN
VLADIAVEAEATIVAMMAGATDNVANGNETEALLRRIGLAAKAYWCKRSTAAAE
ALECIQNGYVEDSGMPRLYREAPLMGMEGSGNVALDTRAMATRPACVEYFDEL
ARSAGODPRLDGHVERLPOLGDLDTIGYRAKIAEDICLALQGSILVRHGPVAVAA
FLATRLGOMGAGTWPAGLDLAPILERALVKG"
13498. .14436
/gene="MT0702"
13498. .14436
/note="similar to GP:3885480; identified by sequence
similarity; putative"
/codon_start=1
/transl_table=1
/product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK44927.1"
/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKMTYEYTGRIARTFNRPEKGNATIDPPL
ELSLIVERADLDGVHVLVSGRGEFCAGFDLSAYAESSSTNGGAGYOGTYIDCKT
OAVNHLPNOPMDPKIDYQMSRYPFGPASTLMHADKPTVVKIHGCVAGTDLAHADQ
VIAAADKICGPPRWGVPRAGLMAHRLSDQRAKRLFTGDCITGAQAEMWGLAVEA
PEPDLDETERLVARIALPVLNOLIMVKLALNSALLQGVATSRMSTVFDEGAARHT
PEGHAFVADAVEHGFDAVRRDPEFGDYRQASRV"
14439. .15161
/gene="MT0703"
14439. .15161
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"

Query Match 100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcgttcgatgaacc 20
|||||
Db 1709 TACGGCGTTTCGATGACC 1690

Search completed: August 7, 2002, 23:49:03
Job time: 9217 sec

CC compared to the cleavage products of reference gene sequences. The
 CC method is used for detecting mutation in the human p53 gene; for
 CC identifying strains of microorganisms, especially bacteria selected
 CC from the group of members of the genera Campylobacter,
 CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
 CC The method may also be used for the identification of viruses,
 CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
 CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
 CC region of the Mycobacterium tuberculosis rpoB gene, which, when
 CC mutated is associated with rifampin resistance. The 620 bp region
 CC amplified spans both the H451Y and S456L mutations. The amplified
 CC fragments are given in AAT29124 (wild type) and AAT29125-26
 CC (mutant sequences).

CC Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgaacc 20
 ||||||||||||||||
 Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 8

AAT09676/C
 ID AAT09676 standard; DNA: 970 BP.

AC AAT09676;

DT 15-OCT-1996 (first entry)

XX Mycobacterium tuberculosis rpoB gene DNA sequence.

XX Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;

KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers

FH primer_bind 10..27

FT /tag= a

FT /note= "primer FENLFP"

FT primer_bind 226..243

FT /tag= b

FT /note= "primer DDIDL"

FT primer_bind 226..240

FT /tag= c

FT /note= "primer DDIDL"

FT primer_bind 338..364

FT /tag= d

FT /note= "primer rpo95"

FT primer_bind 348..373

FT /tag= e

FT /note= "primer rpo105"

FT primer_bind 354..373

FT /tag= f

FT /note= "primer KY290"

FT primer_bind 372..373

FT /tag= g

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind 433..434

FT /tag= h

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind 438

FT /tag= i

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind 468..469

FT /tag= j

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /tag= k
 FT /note= "M. tuberculosis signature nucleotide"
 FT misc_feature 501
 FT /tag= l
 FT /note= "M. tuberculosis signature nucleotide"
 FT misc_feature 516
 FT /tag= m
 FT /note= "M. tuberculosis signature nucleotide"
 FT primer_bind 516..535
 FT /tag= n
 FT /note= "primer rpo273"
 FT misc_feature 525
 FT /tag= o
 FT /note= "M. tuberculosis signature nucleotide"
 FT primer_bind 525..541
 FT /tag= p
 FT /note= "primer KY292"
 FT primer_bind 536..562
 FT /tag= q
 FT /note= "primer rpo293"
 FT primer_bind 640..666
 FT /tag= r
 FT /note= "primer rpo397"
 FT primer_bind 952..966
 FT /tag= s
 FT /note= "primer NMORQ-1"
 FT primer_bind 952..966
 FT /tag= t
 FT /note= "primer NMORQ-2"

MO9533074-A1.

PD 07-DEC-1995.

XX 26-MAY-1995; 95WO-US06790.

XX 26-MAY-1994; 94US-0250030.

XX (HOFF) HOFFMANN LA ROCHE INC.

PA (MAYO-) MAYO FOUNDATION.

XX Felnlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;

XX Young KKY;

XX WPI; 1996-030581/03.

XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA

XX with a primer set that targets portions of the gene encoding rpoB.

XX Disclosure: Fig.3; 54pp; English.

CC This oligonucleotide DNA primer is specific for Mycobacterium
 CC tuberculosis, and may be used to amplify a sample DNA by targeting
 CC a portion of the gene encoding rpoB. The 1st several bases comprise a
 CC nonhybridizing tail consisting of filler bases followed by
 CC a restriction site incorporated to facilitate cloning using the
 CC amplicon at a later date, if desired. The remaining bases hybridize
 CC to bacterial rpoB DNA. The method provides for the detection of M.
 CC tuberculosis and the concurrent determination of its drug
 CC susceptibility, particularly to rifampin. The method can provide
 CC often greater than 95% sensitivity and 100% specificity. The
 CC biological sample is a fluid or tissue sample from a human.

CC Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 970;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgaacc 20
 ||||||||||||||||
 Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 9
AAH51976/c
ID AAH51976 standard; DNA: 3519 BP.
XX
XX
AC AAH51976;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KM Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
XX
PR 12-NOV-1999; 99US-0165124.
XX
PR 01-FEB-2000; 2000US-0179531.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI: 2001-329193/34.
DR P-PSDB; AAG81125.
XX
XX
PT Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
XX
PS Disclosure: Page 68-69; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 1529 TACGGCGTTTCGATGAACCC 1510

RESULT 10
AAH02079/c
ID AAH02079 standard; DNA: 3534 BP.
XX
AC AAH02079;
XX
DT 24-JUL-2001 (first entry)

XX
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
XX Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
XX
OS Mycobacterium tuberculosis.
XX
PN W0200123604-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000WO-CA01150.
XX
XX 28-SEP-1999; 99CA-2283458.
XX
XX 19-MAY-2000; 2000CA-2307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI: 2001-245006/25.
XX
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
XX
XX
PS Disclosure: Page 1478-1479; 1580pp; English.
XX
XX The present invention describes a method for generating a repertoire of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 1547 TACGGCGTTTCGATGAACCC 1528

RESULT 11


```

AAA74651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PI particularly for detecting rifampin resistance in Mycobacterium
XX tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
DB 2122 TACGGCGCTTCGATGAACCC 2103
|||||
RESULT 12
ID AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
PI

```

```

PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PI Mycobacterium, comprising detecting mutations in a gene and relating
XX them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

```

```

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
DB 2122 TACGGCGCTTCGATGAACCC 2103
|||||
RESULT 13
ID AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Mechelinx L, Portels F;

```

```

PI Rosau R;
XX WPI: 1996-040250/04.
XX
XX Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
XX Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
CC
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;

Query Match      95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 19
   |||
Db 1 tacggcgttcgatgaacc 19

RESULT 14
AAT09670
ID AAT09670 standard; DNA; 27 BP.
XX
AC AAT09670;
XX
XX 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
KM Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Synthetic.
XX
PN W09533074-A1.
XX
PD 07-DEC-1995.
XX
PF 26-MAY-1995; 95WO-US06790.
XX
PR 26-MAY-1994; 94US-0250030.
XX
PA (HOFF ) HOFFMANN LA ROCHE INC.
PA (MAYO-) MAYO FOUNDATION.
XX
PI Feinlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
PI Young KKY;
XX
XX WPI: 1996-030581/03.
XX
PT Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT with a primer set that targets portions of the gene encoding rpoB.
XX
XX Claim 9; Page 39; 54pp; English.
XX
CC This oligonucleotide DNA primer is specific for Mycobacterium
CC tuberculosis, and may be used to amplify a sample DNA by targeting
CC a portion of the gene encoding rpoB. The method provides for the

```

```

CC detection of M. tuberculosis and the concurrent determination of its
CC drug susceptibility, particularly to rifampicin. The method can
CC provide often greater than 95% sensitivity and 100% specificity.
CC The biological sample is a fluid or tissue sample from a human.
XX
SQ Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other;

Query Match      75.0%; Score 15; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
   |||
Db 1 cgttcgatgaacc 15

RESULT 15
AA051532/C
ID AA051532 standard; DNA; 3447 BP.
XX
AC AA051532;
XX
XX 17-MAY-1994 (first entry)
XX
DE M. leprae rpoB gene.
XX
KM rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
XX Mycobacterium leprae.
XX
XX
XX Key Location/Qualifiers
FH 1..3447
FT /*tag= a
FT /*note= "rifampicin-sensitive; in resistant
FT strains the Ser codon (TGC at
FT nucleotides 1273-1275) is often mutated
FT to a Phe, Met or esp. Leu codon"
XX
XX W09322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASST-) ASSISTANCE PUBLIQUE.
PA (INSP ) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
XX WPI: 1993-36812/46.
XX
DR P-PSDB; AAR43671.
XX
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
XX isoniazid, rifampicin or streptomycin resistance in tuberculosis
XX by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Fig 12; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. A common

```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
 CC substituted, most frequently by Leu.
 XX
 SO Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gttcgaatgaacc 20
 |||||||||
 Db 1448 GTTCGATGAACCC 1435

Search completed: August 8, 2002, 00:01:26
 Job time: 7615 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:33 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 taacgcgttcgatgacc 20

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	17	85.0	234	10 W06754	W06754 S
2	17	85.0	579	10 T24127	T24127 S
3	16	80.0	624	10 BE896357	BE896357 S
4	15	75.0	384	10 BM077908	BM077908 S
5	15	75.0	452	9 AW694629	AW694629 S
6	15	75.0	517	12 TA247H04P	TA247H04P S
7	15	75.0	536	12 A0783856	A0783856 S
8	15	75.0	537	12 TA140G03P	TA140G03P S
9	15	75.0	540	12 TA190A10P	TA190A10P S
10	15	75.0	631	12 BH615799	BH615799 S
11	15	75.0	690	9 BE053145	BE053145 S
12	15	75.0	1033	12 CNS040XP	CNS040XP S
13	15	75.0	1218	10 BM007170	BM007170 S
14	14	70.0	247	9 AV640031	AV640031 S
15	14	70.0	269	9 AV640876	AV640876 S
16	14	70.0	288	9 BB177553	BB177553 S
17	14	70.0	336	12 A0660540	A0660540 S

C	18	14	70.0	390	9	AV644609	AV644609
C	19	14	70.0	416	9	AJ284239	AJ284239
C	20	14	70.0	421	12	A2813806	A2813806
C	21	14	70.0	428	10	BK252718	BK252718
C	22	14	70.0	431	9	AW280184	AW280184
C	23	14	70.0	466	9	AF051116	AF051116
C	24	14	70.0	472	10	BE449520	BE449520
C	25	14	70.0	474	9	AV396989	AV396989
C	26	14	70.0	476	9	A1483656	A1483656
C	27	14	70.0	477	9	A1488127	A1488127
C	28	14	70.0	489	9	AW618736	AW618736
C	29	14	70.0	497	9	AV643117	AV643117
C	30	14	70.0	508	9	AV642711	AV642711
C	31	14	70.0	518	9	AV642141	AV642141
C	32	14	70.0	525	9	AV650840	AV650840
C	33	14	70.0	531	9	AV642766	AV642766
C	34	14	70.0	544	12	A0843909	A0843909
C	35	14	70.0	556	9	AM155814	AM155814
C	36	14	70.0	562	12	BH487728	BH487728
C	37	14	70.0	566	9	AV631818	AV631818
C	38	14	70.0	582	12	CNS01K68	CNS01K68
C	39	14	70.0	626	9	AM442770	AM442770
C	40	14	70.0	626	9	BB640393	BB640393
C	41	14	70.0	628	10	BF270176	BF270176
C	42	14	70.0	664	10	BG102752	BG102752
C	43	14	70.0	670	12	A0943645	A0943645
C	44	14	70.0	672	12	A0943372	A0943372
C	45	14	70.0	676	9	A1491107	A1491107

ALIGNMENTS

RESULT 1
W06754/c 234 bp mRNA linear EST 01-JUL-1996
LOCUS SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754 GI:1444974
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeididae; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Franco,G.R. and Pena,S.D.J.
TITLE Unpublished
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
Location/Qualifiers
1..234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria
Franco"

/lab_host="DH10B, JM109"
/note="Vector: BA vector, Site_1: NotI, Site_2: HindIII;
Total cellular RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
Guandine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (Jaefmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells."

BASE COUNT 49 a 84 c 66 g 33 t 2 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaa 17
|||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 2

T24127/c T24127 579 bp mRNA linear EST 27-FEB-1995
DEFINITION SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco
LOCUS T24127 Schistosoma mansoni cDNA SMPBC65 3', mRNA sequence.
ACCESSION T24127 GI:529730
VERSION T24127.1
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.

REFERENCE

1 (bases 1 to 579)
Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C. and Pena, S.D.J.
Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library

JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward
Location/Qualifiers

FEATURES

Source

1. 579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site 1: NotI; Site 2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdeline, L. M. Biofeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (Jaefmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells."

BASE COUNT 102 a 206 c 179 g 88 t 4 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaa 17
|||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 3

BE896357 BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5', mRNA sequence.
DEFINITION BE896357
ACCESSION BE896357 GI:10360678
VERSION BE896357.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 624)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LIA9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers

FEATURES

Source

1. 624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 155 a 209 c 150 g 110 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ggcgttcgatgaacc 20
|||||
Db 582 GCGTTTCGATGAACCC 597

RESULT 4
 BM077908 384 bp mRNA linear EST 14-NOV-2001
 LOCUS p21a06.y1 Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chlapelli
 DEFINITION McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
 ACCSSION BM077908
 VERSION BM077908.1 GI:16924944
 KEYWORDS EST, hookworm.
 SOURCE Ancylostoma caninum
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS McCarter,J., Clifton,S., Chlapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Pearson,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was constructed by Claire Murphy, Brandt Chlapelli, and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center.
 FEATURES
 source Location/Qualifiers
 1..384
 /organism="Ancylostoma caninum"
 /db_xref="taxon:29170"
 /clone_lib="Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chlapelli McCarter"
 /dev_stage="Serum stimulated L3"
 /lab_host="DH10B"
 /note="Vector: PCRIT-TOPO (Invitrogen); Site1: EcoRI, Site2: EcoRI; The library was constructed by Claire Murphy, Brandt Chlapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Ancylostoma caninum SS/L3 cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCRIT-TOPO(Invitrogen) following the TOPO TA cloning protocol. Nematodes were provided by Dr. Prema Arasu (Prema.Arasu@ncsu.edu) of North Carolina State University in Raleigh, NC."

BASE COUNT 116 a 71 c 85 g 112 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 10; Length 384;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 ggcgttcgatgaac 18
 Db 324 GGCCTTCGATGAC 338
 RESULT 5
 AM694629 452 bp mRNA linear EST 21-DEC-2000
 LOCUS NC078E03ST11021 Developing stem Medicago truncatula cDNA clone
 DEFINITION NC078E03ST 5', mRNA sequence.
 ACCSSION AM694629
 VERSION AM694629.2 GI:11957636

KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 REFERENCE 1 (bases 1 to 452)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7569391.
 CONTACT: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
 Insert Length: 736 Std Error: 0.00
 Plate: 078 row: E column: 03
 Seq primer: TCACACGAAGAAGCATATGAC.
 FEATURES
 source Location/Qualifiers
 1..452
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF078E03ST"
 /clone_lib="developing stem"
 /tissue_type="stem"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
 BASE COUNT 152 a 94 c 91 g 115 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 9; Length 452;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 cgttcgatgaacc 20
 Db 338 CGTTTCGATGAACC 324
 RESULT 6
 TA247H04P 517 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 247h04, forward sequence, genomic survey sequence.
 ACCSSION AL483262
 VERSION AL483262.1 GI:11848938
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 REFERENCE 1 (bases 1 to 517)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
source
1. 517
Location/Qualifiers

/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"

BASE COUNT 116 a 116 c 135 g 150 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgac 18
|||||
Db 293 GCGCTTCGATGAC 307

RESULT 7

AQ783856 536 bp DNA linear GSS 03-AUG-1999
LOCUS
DEFINITION HS.2001.A2.F09.T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.

ACCESSION AQ783856
VERSION
KEYWORDS GSS:
ORGANISM human.

SOURCE

REFERENCE

AUTHORS

Hood, L., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and Keller, A., Smith, J.C., Swartzell, S., Holzman, T., Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., (bases 1 to 536)

1 (bases 1 to 536)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887

Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2001 row: K column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 536.

FEATURES
source
1. 536
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2001 Col=18 Row=K"
/clone.lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"

/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 160 a 124 c 92 g 156 t 4 others
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaccc 20
|||||
Db 506 CGTTTCGATGACCC 520

RESULT 8

TA140G03P 537 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 140g03, forward sequence, genomic survey sequence.

ACCESSION AL466454
VERSION AL466454.1 GI:11835809
KEYWORDS GSS:
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma
1 (bases 1 to 537)

REFERENCE

AUTHORS

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 CITat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

Location/Qualifiers
1. 537
Location/Qualifiers

/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="140g03"

BASE COUNT 108 a 120 c 110 g 199 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 537;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgac 18
|||||
Db 85 GCGCTTCGATGAC 99

RESULT 9

TA190A10P/c 540 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 190a10, forward sequence, genomic survey sequence.

ACCESSION AL477985
VERSION AL477985.1 GI:11841795
KEYWORDS GSS:
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma
1 (bases 1 to 540)

Trypanosoma
1 (bases 1 to 540)

REFERENCE 1 (bases 1 to 540)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhle@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
 FEATURES
 source Location/Qualifiers
 1..540
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="190a10"
 BASE COUNT 177 a 118 c 126 g 119 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 540;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ggcgttcgatgaac 18
 |||||
 DB 325 GCGCTTCGATGAC 311
 RESULT 10
 BH615799 631 bp DNA linear GSS 28-JAN-2002
 LOCUS BMBAC304F01SP6_psu Brugia malayi Genomic Bac Library 3 Brugia
 DEFINITION malayi genomic, DNA sequence.
 ACCESSION BH615799
 VERSION BH615799.1 GI:18380487
 KEYWORDS GSS.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Splturida; Filarioidae;
 Onchocercidae; Brugia.
 1 (bases 1 to 631)
 Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
 J., Guillano, D., Slatko, B. and Blaxter, M.
 Genome survey sequences from the human parasitic nematode Brugia
 malayi
 TITLE Unpublished (2000)
 JOURNAL Contact: Blaxter ML
 COMMENT Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3JF, UK
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ed.ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire
 Whitton and Dr Mike Quail. The sequence was generated by The
 Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
 collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
 Edinburgh, UK.
 Seq primer: SP6 (ATTAGCTGACACTATAG)
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..631
 /organism="Brugia malayi"
 /strain="TBS"
 /db_xref="taxon:6279"
 /clone_lib="Brugia malayi Genomic Bac Library 3"
 /sex="Mixed (male and female)"
 /tissue_type="whole parasite"
 /dev_stage="microfilaria (L1)"
 /note="Vector: pBACE3.6; Site_1: BamH I; Brugia malayi
 genomic DNA was partially cleaved with Sau3A I and size
 fractionated. 7,392 clones were generated by Claire
 Whitton, Blaxter Nematode Genetics Lab, University of
 Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
 Unit, The Sanger Centre, Cambridge, UK."
 BASE COUNT 196 a 94 c 142 g 199 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 631;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 acggcgttcgatga 16
 |||||
 DB 606 ACCGCGTTGCGATGA 620
 RESULT 11
 BE053145 690 bp mRNA linear EST 07-MAR-2001
 LOCUS GA_Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
 DEFINITION arboreum cDNA clone GA_Ea0002K16f, mRNA sequence.
 ACCESSION BE053145
 VERSION BE053145.2 GI:13244065
 KEYWORDS EST.
 SOURCE Gossypium arboreum.
 ORGANISM Gossypium arboreum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 690)
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
 D., Wood, T.C., Leslie, A. and Wilkins, T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 TITLE Unpublished (2000)
 JOURNAL On Jun 8, 2000 this sequence version replaced gi:8380201.
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Seq primer: TAATGACTGACTATAGGG
 High quality sequence stop: 550.
 FEATURES
 source Location/Qualifiers
 1..690
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone_lib="GA_Ea0002K16f"
 /tissue_type="Fibers isolated from bolls harvested 7-10
 dpa"
 /lab_host="E. coli"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 169 a 132 c 151 g 236 t
 2 others

Query Match 75.0%; Score 15; DB 9; Length 690;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggcgttcgatgaac 18
|||||
Db 567 GGCCTTCGATGAC 581

RESULT 12
CNS040Y/C 1033 bp DNA linear GSS 18-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
DEFINITION 073004 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL269530.1 GI:7991421
VERSION 1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1033)
AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Filames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1033)
AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Filames,C., Wincker,P., Brotlier,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1033)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..1033
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="073004"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG073BH02LP1-end : T7"
BASE COUNT 270 a 222 c 276 g 261 t 4 others
ORIGIN
Query Match 75.0%; Score 15; DB 12; Length 1033;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cggcgttcgatgaac 17
|||||
Db 460 CGGCTTCGATGAA 446

RESULT 13
BM007170 1218 bp mRNA linear EST 30-OCT-2001
LOCUS 603614933N1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420816 3',
DEFINITION mRNA sequence.
ACCESSION BM007170

VERSION BM007170.1 GI:16521524
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1218)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM1876 row: a column: 09
High quality sequence start: 25
High quality sequence stop: 313.
Location/Qualifiers
1..1218
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5420816"
/clone_1lb="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(6). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library." 4 others
BASE COUNT 370 a 446 c 244 g 154 t
ORIGIN
Query Match 75.0%; Score 15; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaaccc 20
|||||
Db 364 CGTTCGATGATGCC 378

RESULT 14
AV640031/c 247 bp mRNA linear EST 15-DEC-2000
LOCUS AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
DEFINITION cDNA clone HCL009D4_r 5', mRNA sequence.
ACCESSION AV640031
VERSION AV640031.1 GI:10783359
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 247)
AUTHORS Asamizu,E., Miura,K., Kuchio,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.
 Location/Qualifiers

FEATURES
 Source

1. 247
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone="HCL009b04_r"
 /clone_lib="Chlamydomonas reinhardtii 5% CO₂"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; The cDNA library was constructed from cells cultured
 in a medium with bubbling air containing 5% carbon
 dioxide"

BASE COUNT 61 a 79 c 54 g 53 t
 ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
 |||
 Db 245 GGCGTTTCGATGAA 232

RESULT 15
 AV640876/c

LOCUS AV640876 269 bp mRNA linear EST 15-DEC-2000
 DEFINITION AV640876 Chlamydomonas reinhardtii 5% CO₂ Chlamydomonas reinhardtii
 CDNA clone HCL024a01_r 5', mRNA sequence.

ACCESSION AV640876
 VERSION AV640876.1 GI:10784204
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 269)
 Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
 Nakamura, Y. and Tabata, S.
 Generation of expressed sequence tags from low-CO₂ and high-CO₂
 adapted cells of Chlamydomonas reinhardtii

TITLE
 JOURNAL DNA Res. 7 (5), 305-307 (2000)
 MEDLINE 20539644
 COMMENT

Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.
 Location/Qualifiers

FEATURES
 Source

1. 269
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone="HCL024a01_r"
 /clone_lib="Chlamydomonas reinhardtii 5% CO₂"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; The cDNA library was constructed from cells cultured
 in a medium with bubbling air containing 5% carbon
 dioxide"

BASE COUNT 65 a 85 c 60 g 59 t
 ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
 |||
 Db 254 GGCGTTTCGATGAA 241

Search completed: August 7, 2002, 23:12:33
 Job time: 11072 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
(Without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 tacggcgttcgatgacc 20

Scoring table: IDENTITY_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA_*
1: /cgn2_6/prodata/2/lna/5A_COMB.seq.*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq.*
3: /cgn2_6/prodata/2/lna/6A_COMB.seq.*
4: /cgn2_6/prodata/2/lna/6B_COMB.seq.*
5: /cgn2_6/prodata/2/lna/PCTUS_COMB.seq.*
6: /cgn2_6/prodata/2/lna/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
C 2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
C 3	20	100.0	630	2	US-08-757-653-135	Sequence 135, App
C 4	20	100.0	630	2	US-08-757-653-136	Sequence 136, App
C 5	20	100.0	630	2	US-08-757-653-137	Sequence 137, App
C 6	20	100.0	630	2	US-08-757-653-138	Sequence 138, App
C 7	20	100.0	630	2	US-08-757-653-139	Sequence 139, App
C 8	20	100.0	630	2	US-08-757-653-140	Sequence 140, App
C 9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
C 10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appl
C 11	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appl
C 12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
C 13	18.4	92.0	3447	2	US-08-313-185-57	Sequence 57, Appl
C 14	18.4	92.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
C 15	15.8	79.0	1472	1	US-08-622-354-2	Sequence 2, Appl
C 16	15.8	79.0	2310	1	US-08-622-354-1	Sequence 1, Appl
C 17	15.2	76.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 18	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appl
C 19	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appl
C 20	14.2	71.0	1081	4	US-09-372-422A-33	Sequence 33, Appl
C 21	14.2	71.0	1153	4	US-09-372-448A-5	Sequence 5, Appl
C 22	14.2	71.0	2262	4	US-08-674-887A-5	Sequence 5, Appl
C 23	14.2	71.0	2262	3	US-08-951-844-5	Sequence 5, Appl
C 24	13.8	69.0	117	5	US-08-299-198A-59	Sequence 59, Appl
C 25	13.8	69.0	117	5	PCT-US95-10813-59	Sequence 59, Appl
C 26	13.8	69.0	776	4	US-09-372-422A-43	Sequence 43, Appl
C 27	13.8	69.0	1100	4	US-09-372-422A-47	Sequence 47, Appl

C 28	13.8	69.0	1176	3	US-08-911-853-34	Sequence 34, Appl
C 29	13.8	69.0	1176	4	US-09-479-409-34	Sequence 34, Appl
C 30	13.8	69.0	1176	4	US-09-479-453-34	Sequence 34, Appl
C 31	13.8	69.0	1375	4	US-09-372-422A-37	Sequence 37, Appl
C 32	13.8	69.0	1485	4	US-09-372-422A-39	Sequence 39, Appl
C 33	13.8	69.0	2394	3	US-09-027-064-1	Sequence 1, Appl
C 34	13.8	69.0	2394	4	US-09-271-815-1	Sequence 1, Appl
C 35	13.8	69.0	17612	3	US-08-911-853-29	Sequence 29, Appl
C 36	13.8	69.0	17612	4	US-08-479-409-29	Sequence 29, Appl
C 37	13.8	69.0	17612	4	US-09-479-453-29	Sequence 29, Appl
C 38	13.8	69.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 39	13.6	68.0	585	4	US-09-404-671-3	Sequence 3, Appl
C 40	13.6	68.0	686	4	US-09-372-422A-45	Sequence 45, Appl
C 41	13.6	68.0	699	4	US-08-998-416-705	Sequence 705, Appl
C 42	13.6	68.0	999	4	US-09-177-234-7	Sequence 7, Appl
C 43	13.6	68.0	1087	4	US-09-372-422A-29	Sequence 29, Appl
C 44	13.6	68.0	1209	1	US-08-314-309A-5	Sequence 5, Appl
C 45	13.6	68.0	1513	1	US-08-314-309A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
US-09-082-614A-59/C

; Sequence 59, Application US/09082614A

; Patent No. 6124098

; GENERAL INFORMATION:

; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenti, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

; TITLE OF INVENTION: In Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flanegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082,614A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/313,185

; FILING DATE: 12-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-09-082-614A-59

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 432;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
US-08-757-653-135/C
; Sequence 135, Application US/08757653
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; INFORMATION FOR SEQ ID NO: 135:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 620 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-757-653-135

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 620;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/C

; Sequence 136, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcglttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/c
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcglttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcglttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94104
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,653
;;
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: FORS-02565
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 139:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-139

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamlchev, Victor I.
; APPLICANT: Lyamlchev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable Pen-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-140

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
US-08-797-812-24/C
; Sequence 24, Application US/08797812
; Patent No. 6228575
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas A.
; APPLICANT: Mack, David
; APPLICANT: Chee, Mark S.
; APPLICANT: Berono, Anthony J.
; APPLICANT: Stryer, Lubert
; APPLICANT: Ghandour, Ghassan
; APPLICANT: Wang, Ching
; TITLE OF INVENTION: Chip-Based Species Identification and
; TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,812
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,765
; FILING DATE: 15-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/629,031
; FILING DATE: 08-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,631
; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,339
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16528X-018550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723

GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M. 33,977

REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.1050S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105M01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138

GENERAL INFORMATION:

APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT

APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657,0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-71

```

```

Query Match          95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 tacggcgcttcgatgaacc 19
Db 1 TACGGCGCTTCGATGAGAAC 19

```

```

RESULT 13
US-08-313-185-57/C
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356,0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-313-185-57

```

```

Query Match          92.0%; Score 18.4; DB 2; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 tacggcgcttcgatgaacc 20
Db 1454 TACGGCTTCGATGAGAAC 1435

```

```

RESULT 14
US-09-082-614A-57/C
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356,0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4400
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-082-614A-57

```

```

Query Match          92.0%; Score 18.4; DB 3; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 tacggcgcttcgatgaacc 20
|||||

```

DB 1454 TACGGTGTTCGATGAACCC 1435

RESULT 15

US-08-622-354-2/c
; Sequence 2, Application US/08622354
; Patent No. 5827518
; GENERAL INFORMATION:
; APPLICANT: WEBB, Bruce A.
; APPLICANT: CUI, Liyang
; TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE
; TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: VA
; COUNTRY: US
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/622,354
; FILING DATE: 27-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 190..1155
; US-08-622-354-2

Query Match 79.0%; Score 15.8; DB 1; Length 1472;
Best Local Similarity 89.5%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tacggcgttcgatgacc 19
||||| ||||| ||||| |||||
DB 1105 TACGGGTTTACATGAACC 1087

Search completed: August 7, 2002, 21:54:25
Job time: 24020 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:21; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 taaggcgttcgtatgaacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	396	10	BF220419 NXCI_146
2	17.4	87.0	399	10	BF169611 NXCI_125
3	17.4	87.0	452	10	BC040291 NXCI_110
4	17.4	87.0	539	9	AA556698 553 LobiO
5	17.4	87.0	545	10	BF777209 NXCI_066
6	17.4	85.0	234	10	W06754 SMEST0390 S
7	17.4	85.0	579	9	T24127 SMEST0325 S
8	16.8	84.0	277	9	AA734164 vs19g12.r
9	16.4	82.0	576	10	BF252921 EST420184
10	16.4	82.0	624	10	BE896357 601439015
11	16.4	82.0	631	12	BH615799 BMAC304F
12	16.4	82.0	961	12	AG141490 Pan trogl
13	15.8	79.0	213	9	AM064407 SP0996 KR
14	15.8	79.0	436	9	AI1496312 s005008.y
15	15.8	79.0	582	12	CNS01K68 Anopheles
16	15.8	79.0	637	10	BC908684 Talr1170D
17	15.8	79.0	650	10	BC908616 Talr1169H

C 18	15.8	79.0	752	12	CNS03678	AL229661 Tetradon
C 19	15.8	79.0	775	12	A2125549	A2125549 OSJNB009
C 20	15.8	79.0	885	12	CNS02B0Q	AL189251 Tetradon
C 21	15.8	79.0	913	10	BF204833	BF204833 60167133
C 22	15.8	79.0	1029	12	CNS0549K	AL320465 Tetradon
C 23	15.8	79.0	1411	10	BI663170	BI663170 603286791
C 24	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
C 25	15.4	77.0	248	10	BC140300	BC140300 EST480742
C 26	15.4	77.0	269	9	AV640876	AV640876 AV640876
C 27	15.4	77.0	384	10	BM077908	BM077908 pb21906.y
C 28	15.4	77.0	467	12	AV644609	AV644609 AV644609
C 29	15.4	77.0	390	10	CNS03FUV	AL242176 Tetradon
C 30	15.4	77.0	474	9	AV396989	AV396989 AV396989
C 31	15.4	77.0	489	9	AM618736	AM618736 EST320722
C 32	15.4	77.0	497	9	AV643117	AV643117 AV643117
C 33	15.4	77.0	508	9	AV642711	AV642711 AV642711
C 34	15.4	77.0	518	9	AV642141	AV642141 AV642141
C 35	15.4	77.0	531	9	AV642766	AV642766 AV642766
C 36	15.4	77.0	532	10	BI506216	BI506216 BI170018A
C 37	15.4	77.0	536	12	AO783856	AO783856 HS_2001.A
C 38	15.4	77.0	548	12	AQ497017	AQ497017 HS_5197.B
C 39	15.4	77.0	566	9	AV631818	AV631818 AV631818
C 40	15.4	77.0	788	10	BE566696	BE566696 601339653
C 41	15.2	76.0	146	10	BM096759	BM096759 EBMA07.SQ
C 42	15.2	76.0	200	10	BM098906	BM098906 EBP105.SQ
C 43	15.2	76.0	205	12	A2577000	A2577000 06D05.SHO
C 44	15.2	76.0	269	10	BF953380	BF953380 RC3-NN019
C 45	15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
LOCUS BF220419 396 bp mRNA linear EST 08-NOV-2000
DEFINITION NXCI_146 A06_F NXCI (Nsif Xylem Compression wood Inclined) Pinus
taeda cDNA clone NXCI_146 A06 5', mRNA sequence.

ACCESSION BF220419.1 GI:11126551

VERSION BF220419.1

KEYWORDS taeda

SOURCE loblolly pine.

ORGANISM Pinus taeda

REFERENCE Sederoff, R.

AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome

TITLE Unpublished (2000)

JOURNAL Contact: Johnson, Arthur

COMMENT North Carolina State University

Tel: 919 515 7800

Fax: 919 515 7801

Email: ajohnson@unity.ncsu.edu

Seq primer: T3

FEATURES

Location/Qualifiers

1..396

/organism="Pinus taeda"

/strain="Coastal plain loblolly pine from North Carolina"

/db_xref="taxon:3352"

/clone="NXCI_146 A06"

/clone_1lb="NXCI (Nsif Xylem Compression wood Inclined)"

/tissue="Xylem"

/cell_type="Compression"

/dev_stage="juvenile"

/lab_host="XLI-Blue"

/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: Xho I

; The library is from early (spring) wood, taken from

three six-year old trees (three different genotypes), in

the juvenile phase. These trees were induced to form

compression wood by bending to a 45 degree angle and tying

them to the ground. Differentiating xylem was harvested

from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGCGACGAG'."

BASE COUNT 71 a 84 c 122 g 110 t 9 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 2
BF169611 399 bp mRNA linear EST 30-OCT-2000
LOCUS NXCI_125_C05_F NXCI (Nsf Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NXCI_125_C05 5', mRNA sequence.
BF169611
ACCESSION BF169611.1 GI:11054228
VERSION
KEYWORDS
SOURCE
ORGANISM
Pinus taeda
loblolly pine.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Basis of Wood Formation in the Pine Megagenome
Published (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..399
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone_1fb="NXCI_125_C05"
/clone_1lb="NXCI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"

/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of
all three genotypes was used for the library. oligo-dT
primed cDNA was directionally cloned into the EcoRI-XhoI
Bluescript SK vector arms. NOTE: The sequences contain a
'cDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTCGCGACGAG'."

BASE COUNT 71 a 84 c 121 g 121 t 2 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||

Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 3
BG040291 452 bp mRNA linear EST 24-JAN-2001
LOCUS NXSI_110_F06_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
DEFINITION clone NXSI_110_F06 5', mRNA sequence.
BG040291
ACCESSION BG040291.1 GI:12482876
VERSION
KEYWORDS
SOURCE
ORGANISM
loblolly pine.
Pinus taeda

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Basis of Wood Formation in the Pine Megagenome
Published (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..452
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone_1fb="NXSI_110_F06"
/clone_1lb="NXSI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"

/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGCGACGAG'."

BASE COUNT 71 a 122 c 146 g 95 t 18 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||
Db 329 ACGGCGCTTCGATGAACCC 347

RESULT 4
AA556698 539 bp mRNA linear EST 28-AUG-1998
LOCUS 553 loblolly pine CA Pinus taeda cDNA clone ICABAG, mRNA sequence.
DEFINITION AA556698
ACCESSION AA556698.1 GI:3365713
VERSION
KEYWORDS
SOURCE
ORGANISM
loblolly pine.
Pinus taeda

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Molecular Basis of Wood Formation in the Pine Megagenome
Published (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

AUTHORS
Allona, I., Quinn, M., Shoop, E., Swope, K., St. Cyr, S., Carlis, J.,
Riedel, J., Retzel, E., Campbell, M.M., Sederoff, R., and Whetten, R.W.
TITLE
Analysis of xylem formation in pine by cDNA sequencing
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
MEDLINE
96356220
COMMENT
Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
Email: rosswhetten@unc.edu

FEATURES
source
1. .539
Location/Qualifiers

BASE COUNT 102 a 120 c 156 g 150 t 11 others
ORIGIN
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="1CAB4G"
/clone_lib="loblolly pine CA"
/tissue_type="xylem"
/lab_host="SOLR"
/note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
The result of subtraction of C library with N library.
Immature xylem from the underside of inclined stems of
differentiating compression wood was substracted with
immature xylem from the side of inclined stems of
differentiating wood. A mixture of four genotypes were
used. Oligo-dT primed cDNA was directionally cloned into
the EcoRI-XhoI lambda-ZAP vector arms"

Query Match 87.0%; Score 17.4; DB 9; Length 539;
Best Local Similarity 94.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 accgagcttcgatgaacc 20
||||| |||||||||
Db 145 ACGGCGCTTCGATGACCC 163

RESULT 5
BF777209 545 bp mRNA linear EST 12-JAN-2001
LOCUS
NLSI_066_E05_F NLSI (Nsf xylem side wood inclined) Pinus taeda cDNA
DEFINITION
clone NLSI_066_E05 5', mRNA sequence.
ACCESSION
BF777209
VERSION
BF777209.1 GI:12125109
KEYWORDS
EST.
SOURCE
loblolly pine.
Pinus taeda
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE
1 (bases 1 to 545)
Sederoff, R.
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unc.edu
Seq primer: T3.

FEATURES
source
1. .545
Location/Qualifiers

/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NLSI_066_E05"
/clone_lib="NLSI (Nsf xylem side wood inclined)"

/tissue_type="xylem"
/cell_type="side"
/dev_stage="juvenile"
/lab_host="XIL-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. Oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'ATTCGCGACGAG'."

BASE COUNT 92 a 142 c 167 g 132 t 12 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 545;
Best Local Similarity 94.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 accgagcttcgatgaacc 20
||||| |||||||||
Db 256 ACGGCGCTTCGATGACCC 274

RESULT 6
W06754 234 bp mRNA linear EST 01-JUL-1996
W06754/c
LOCUS
SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION
Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION
W06754
VERSION
W06754.1 GI:1444974
KEYWORDS
EST.
SOURCE
Schistosoma mansoni.
ORGANISM
Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE
1 (bases 1 to 234)
Franco, G.R. and Pena, S.D.J., Unpublished
AUTHORS
Franco, G.R. and Pena, S.D.J., Unpublished
JOURNAL
Unpublished (1996)
COMMENT
Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Biologia
Inmunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (531)4415611
Fax: (531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.

FEATURES
source
1. .234
Location/Qualifiers

/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
Total cellular RNA from male and female adult worms was
extracted according to a modification (Pulsant, C. and
Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
guanidine thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (lambdafmd BA vector, a phagemid derived from pEMV, Adams, M. D. et al. Nature Genet. 4: 373-389, 1993), and electroporated into *E. coli* strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

Query Match	85.0%	Score 17	DB 10	Length 234
Best Local Similarity	100.0%	Pred. No.	1e+02	
Matches 17	Conservative 0	Mismatches 0	Indels 0	Gaps 0

OY 1 tacggcgttcgatgaa 17
 ||| ||||| ||||| |||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT	7
T24127/c	
LOCUS	579 bp mRNA
DEFINITION	linear EST 27-FEB-1995
ACCESION	U01127
	SMSST0325 Schistosoma mansoni, adult worm, Gloria Franco
	Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
	U01127

SOURCE ORGANISM	Schistosoma mansoni	Schistosoma mansoni
-----------------	---------------------	---------------------

REFERENCE
AUTHORS
1 (bases 1 to 579)
Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.

TITLE	ABSTRACT
Identification of new <i>Schistosoma mansoni</i> genes by the EST strategy using a directional cDNA library	141-147 (1995)
Journal	Gene 152, 141-147 (1995)

COMMENT

Laboratório de Genética-Bioquímica, Departamento de Bioquímica e Imunologia
Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais
Avenida Antônio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010.
Tel.: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.

FEATURES
source

/organism="Schistosoma mansoni"
 /strain="NMRI"
 /db_xref="taxon:6183"
 /clone="SMP65"
 /clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
 /lab_host="DH10B, JM109"
 /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houtbine, L. M. Biofeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (laminid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and electroporated into E. coli strain DH10B (BRL). The

BASE COUNT	ORIGIN
102 a	library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "
206 c	
179 g	
88 t	4 others

Query Match	85.0%;	Score 17;	DB 10;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 1.3e+02;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	taaggcgcttgcgatgaa	17
Db	75	TAACGGCGCTTGCATGAA	59

RESULT	8
AA734164	
LOCUS	277 bp mRNA
DEFINITION	linear EST 07-JAN-1998
	v519q12.r1 Barstead mouse irradiated colon MPRB7 Mus musculus cDNA
	clone IMAGE:1138726 5' similar to gb:X80699 M.musculus L26 mRNA
	(MOUSE):: mRNA sequence.

SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 277)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.

TITLE	JOURNAL	COMMENT
The WashU-HMI Mouse EST Project	Unpublished (1996)	
Contact: Maira M/Mouse EST Project		
Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theisling, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterson, R.		

wustl-nhl mouse bst project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouse@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:619998

FEATURES

source

```
1. 277
   /organism="Mus musculus"
   /strain="FVB/N"
   /db_xref="taxon:10090"
   /clone_image="1138726"
   /clone_id="Bartstead mouse irradiated colon MPLRB7"
   /dev_stage="8 weeks"
   /lab_host="DH10B"
   /note="Vector: pT73d-Pac (Pharmacia) with a modified
polylinker. Site.1: EcoRI; Site.2: NotI. Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
[5'GTTACGATCTCAGATGGAGGCGCCCTTTTCTTTTTTTTTTTTTTTT
T3']; double-stranded cDNA was ligated to Eco RI
adaptors [AATTGGATCTTG], digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library constructed by Bob Bartstead. "
```

BASE COUNT

64 a 59 c 92 g 62 t

Query Match 84.0%; Score 16.8; DB 9; Length 277;
 Best Local Similarity 90.0%; Pred. No. 1.4e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taccgcttcgattgaacc 20
 ||||| ||||| |||||
 Db 47 TACGGCTTTCGATGACCC 66

RESULT 9
 BE252921 576 bp mRNA linear EST 15-NOV-2001
 LOCUS BE252921/c
 DEFINITION Immittis CDNA clone C1ABC49 5' sequence, mRNA sequence.
 ACCESSION BE252921
 VERSION BE252921.1 GI:16933064
 KEYWORDS EST.
 SOURCE Coccidioides Immittis.
 ORGANISM Coccidioides Immittis.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 Onygenales; Microsporite Onygenales; Coccidioides.

REFERENCE 1 (bases 1 to 576)
 AUTHORS Gardner, M.J., and Kirkland, T.
 TITLE Generation of ESTs from Coccidioides Immittis spherule CDNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Malcolm J. Gardner
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301 838 3519
 Fax: 301 838 0208
 Email: gardner@tigr.org.
 Location/Qualifiers
 1..576
 /organism="Coccidioides Immittis"
 /db_xref="taxon:5501"
 /clone="C1ABC49"
 /clone_1lb="Coccidioides Immittis spherule CDNA library"
 /dev_stage="spherule"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 113 a 186 c 176 g 101 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 576;
 Best Local Similarity 94.4%; Pred. No. 2.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 cggcgcttcgattgaacc 20
 ||||| ||||| |||||
 Db 241 CGCGCTTCGATGACCC 224

RESULT 10
 BE896357 624 bp mRNA linear EST 20-OCT-2000
 LOCUS BE896357
 DEFINITION 601439015F1 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:3924266 5',
 mRNA sequence.
 ACCESSION BE896357
 VERSION BE896357.1 GI:10360678
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 624)
 NIH-MGC http://mgc.ncl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCPD/DRP
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LAM8761 row: m column: 03
 High quality sequence start: 2
 High quality sequence stop: 403.
 Location/Qualifiers
 1..624
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3924266"
 /clone_1lb="NIH_MGC_72"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

BASE COUNT 155 a 209 c 150 g 110 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 624;
 Best Local Similarity 94.4%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 cggcgcttcgattgaacc 20
 ||||| ||||| |||||
 Db 580 CGCGCTTCGATGACCC 597

RESULT 11
 BH615799 631 bp DNA linear GSS 28-JAN-2002
 LOCUS BH615799
 DEFINITION BMBAC304F01SP6_P5U Brugia malayi genomic BAC library 3 Brugia
 malayi genomic, DNA sequence.
 ACCESSION BH615799
 VERSION BH615799.1 GI:18380487
 KEYWORDS GSS.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 631)
 Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
 'J., Guilliano, D., Slatko, B. and Blaxter, M.
 Genome survey sequences from the human parasitic nematode Brugia
 malayi
 Unpublished (2000)
 Contact: Blaxter ML
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3J7, UK
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire
 Whitton and Dr Mike Quail. The sequence was generated by The
 Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
 collaboration with Mark Blaxter, ICAAP, University of Edinburgh,
 Edinburgh, UK.
 Seq primer: SP6 (ATTAGTACACACTATAG)
 Class: BAC ends.
 Location/Qualifiers
 1..631
 /organism="Brugia malayi"

FEATURES
 source

/strain="TRS"
/db_xref="taxon:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBAC3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size -48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

BASE COUNT 196 a 94 c 142 g 199 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 631;
Best local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 19
|||||
Db 606 ACGCGCTTCGATGATCC 623

RESULT 12
AG141490 961 bp DNA linear GSS 08-JAN-2002
LOCUS AG141490/c Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG141490
VERSION AG141490.1 GI:16671168
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RP43-Chimpanzee
ORGANISM Male BAC library clone:RP43-001J13.TJ.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (sites)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library RP43-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 961)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbgs@sc.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RP43-43 This BAC end was generated during the Rsp process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : SCORI
R.Site 2 : SCORI
Location/Qualifiers
1. 961
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone_lib="RP43-001J13.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP43-Chimpanzee Male BAC Library"
BASE COUNT 255 a 299 c 145 g 252 t 10 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 961;
Best local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 19
|||||
Db 746 ACGCGCTTCGATGATACC 729

RESULT 13
AM064407 213 bp mRNA linear EST 07-DEC-2000
LOCUS AM064407/c SP0996 KRIIB Human CD4 Intrathymic T-cell cDNA library Homo sapiens
DEFINITION cDNA 3', mRNA sequence.
ACCESSION AM064407
VERSION AM064407.1 GI:8888344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 213)
AUTHORS Goh, S.-H., Park, J.-H., Lee, Y.-S., Lee, H.-G., Yoo, H.-S., Lee, I.-C., Park, J.-H., Kim, Y.-S. and Lee, C.-C.
TITLE Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis
JOURNAL Genomics 70 (1), 1-18 (2000)
MEDLINE 20541704
COMMENT Contact: Sung-Ho Goh
Genome Center
Korea Research Institute of Bioscience and Biotechnology
Oun-dong 52, Yu Sung-gu, Daejeon 305-353, Republic of Korea
Tel: 82-42-860-4473
Fax: 82-42-860-4479
Email: gohsh@mail.kribb.re.kr
Seg primer: T7
High quality sequence stop: 213
POLYA-No.

FEATURES
source Location/Qualifiers
1. 213
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KRIIB Human CD4 Intrathymic T-cell cDNA library"
/tissue_type="thymus"
/cell_type="intrathymic T-cell"
/dev_stage="CD3+4+8- single positive stage"
/note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3+4+8-T-cell, adaptor ligated, amplified with PCR, and cloned into pGEM-T vector."

BASE COUNT 41 a 59 c 72 g 40 t 1 others
ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 213;
Best local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
|||||
Db 43 ACGCGCTTCGATGATACC 25

RESULT 14
A1496312 436 bp mRNA linear EST 30-NOV-2001
LOCUS sb05b08.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl004-7888 5' similar to TR:Q92388 Q92388 CNG1 GENE. ;, mRNA sequence.
ACCESSION A1496312

VERSION	AI496312.1	GI:4397315
KEYWORDS	EST.	
SOURCE	soybean.	
ORGANISM	Glycine max	
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes: Magnoliophyta; eudicotyledons: core eudicots: Rosidae: eucroside I; Fabales: Fabaceae; Papilionoideae; Phaseoleae; Glycine.	
AUTHORS	1 (bases 1 to 436)	
TITLE	Shoemaker, R., Keim, P., Vocklin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, B., Allent, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	
JOURNAL	Public Soybean EST Project	
COMMENT	Unpublished (1999) Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Seq primer: -40RP from Gldco High quality sequence stop: 386 POLYA-No.	
FEATURES	Location/Qualifiers	
SOURCE	1..436	
	/organism="Glycine max"	
	/db_xref="taxon:3847"	
	/clone="GENOME SYSTEMS CLONE ID: Gm-cl004-7888"	
	/clone_1bp="Gm-cl004"	
	/issue_type="root"	
	/lab_host="XL10-gold"	
	/note="Vector: pluescript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGACAGACAGACAGACAGACACGACG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone pfu DNA polymerase, ligated to EcoRI adaptors, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA size fractionation column. The column eluent was then ligated into Stratagene's pluescript II XR predigested vector (pluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"	
BASE COUNT	90 a	174 c 96 g 76 t
ORIGIN		
Query Match	79.0%	Score 15.8; DB 9; Length 436;
Best Local Similarity	89.5%;	Pred. NO. 5.3e+02;

```

Matches 17, Conservative 0; Mismatches 2; Indels 0; Gaps 0.
OY 2 acgcgcttcgatgaacc 20
    ||| ||| ||||| |||||
Db 185 ACGCGCTCTCGATGAACC 203

RESULT 15
CONSOLK68/c 582 bp DNA linear GSS 12-JUN-2001
LOCUS
DEFINITION Anopheles gambiae GSS sp6 end of clone 16E18 of NotreDame1 library
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
AL147937
ACCESSION AL147937.1 GI:7006083
VERSION
KEYWORDS
SOURCE
ORGANISM
            African malaria mosquito.
            Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
            Culicoidae; Anopheles.
            1 (bases 1 to 582)
REFERENCE
            Genoscope.
            Direct Submision
            Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            2 (bases 1 to 582)
            Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
            Direct Submision
            Submitted (16-FEB-2000) BWHI, Institut Pasteur, 25, rue du Dr.
            Roux, Paris 75015, France
COMMENT
            This clone is from an A. gambiae BAC library provided by F.H.
            Collins and sequenced by Genoscope in collaboration with the
            Laboratory of Biochem. and Biol. Molec. of Insects, Institut
            Pasteur.
FEATURES
            source
            1..582
            /organism="Anopheles gambiae"
            /strain="PEST"
            /db_xref="taxon:7165"
            /clone="16E18"
            /clone_1ib="Notredame1"
            /note="end : SP6"
BASE COUNT 160 a 124 c 136 g 153 t 9 others
ORIGIN

Query Match 79.0%; Score 15.8; DB 12; Length 582;
Best Local Similarity 89.5%; Pred. No. 5,7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0.
OY 2 acgcgcttcgatgaacc 20
    ||| ||| ||||| |||||
Db 320 ACGCGCTTCGATGAACC 302

Search completed: August 7, 2002, 21:15:21
Job time: 22891 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20
Sequence: 1 tacggcgttcgataaaccc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802.*

1:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20	AAA49824
2	20	100.0	20	AAA49826
3	20	100.0	432	AAO61457
4	20	100.0	480	AAA49863
5	20	100.0	620	AAAT29126
6	20	100.0	620	AAAT29124
7	20	100.0	970	AAAT29125
8	20	100.0	970	AAAT09676
9	20	100.0	3519	AAH51976

C	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
C	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
C	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
C	13	19	95.0	19	17	AAAT12096	M. tuberculosis rp
C	14	18.4	92.0	3447	14	AAO51532	M. leprae rpoB gene
C	15	16.8	84.0	3474	23	AAO51357	Enterococcus faeca
C	16	16.8	84.0	3624	23	AAO52892	Enterococcus faeca
C	17	16.8	84.0	9179	20	AAAT13246	C. glutamicum SRT
C	18	15.4	77.0	612	22	AAAT71082	C. glutamicum SRT
C	19	15.4	77.0	1344	22	AAH68297	C. glutamicum codin
C	20	15.4	77.0	6275	24	AB132551	Human immune syste
C	21	15.4	77.0	309400	22	AAH68534	C. glutamicum codin
C	22	15.2	76.0	1446	21	AAAC42071	Arabidopsis thalia
C	23	15.2	76.0	2853	23	AB112631	Drosophila melanog
C	24	15.2	76.0	3276	23	AB102493	Drosophila melanog
C	25	15.2	76.0	4505	21	AAAT15009	Nucleotide sequenc
C	26	15.2	76.0	5574	23	AB102492	Drosophila melanog
C	27	15.2	76.0	7243	23	AB102521	Drosophila melanog
C	28	15.2	76.0	8193	23	AB112630	Drosophila melanog
C	29	15.2	76.0	21748	23	AB102520	Drosophila melanog
C	30	15.2	76.0	27426	23	AAO59541	Protonibacterium
C	31	15.2	76.0	4403765	22	AAI99683	Mycobacterium tube
C	32	15	75.0	27	17	AAAT09670	Mycobacterium tube
C	33	14.8	74.0	822	23	AAO54258	Pseudomonas aerugi
C	34	14.8	74.0	894	23	AAO51512	Pseudomonas aerugi
C	35	14.8	74.0	1167	22	AAAT81355	Quorum sensing con
C	36	14.8	74.0	2176	15	AAO57017	PKC nu. Bos tauru
C	37	14.4	72.0	1014	22	AAH65487	C. glutamicum codin
C	38	14.4	72.0	1086	23	AAO593170	DNA encoding novel
C	39	14.4	72.0	1086	23	AAO593247	DNA encoding novel
C	40	14.4	72.0	1578	21	AAO48875	Arabidopsis thalia
C	41	14.4	72.0	1579	21	AAO40928	Arabidopsis thalia
C	42	14.4	72.0	2660	23	AB110327	Drosophila melanog
C	43	14.4	72.0	3342	23	AB112342	Drosophila melanog
C	44	14.4	72.0	3362	23	AB117225	Drosophila melanog
C	45	14.4	72.0	3632	23	AB113365	Drosophila melanog

ALIGNMENTS

RESULT 1

ID	AAA49824	standard; DNA: 20 BP.
XX	AAA49824;	
AC	25-SEP-2000	(first entry)
DT	Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.	
XX	Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;	
KW	ss.	
XX	Mycobacterium tuberculosis.	
OS	WO200036142-A1.	
PN	22-JUN-2000.	
XX	10-DEC-1999:	99MO-CA01177.
PF	11-DEC-1998:	98US-0111794.
PR	(VIST-) VISIBLE GENETICS INC.	
XX	Shipman R;	
PA	WPI: 2000-431611/37.	
PI	Method for the detection and characterization of Mycobacterium	
XX	tuberculosis with antibiotic resistance in a sample -	

PS Claim 4; Page 4; 43pp; English.

XX
CC The present sequence is that of the *Mycobacterium tuberculosis*
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 1 tacggcggttcgatgaacc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA; 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE *Mycobacterium tuberculosis* rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PE 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of *Mycobacterium*
XX tuberculosis with antibiotic resistance in a sample -
PS Claim 4; Page 5; 43pp; English.
XX
XX The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 1 tacggcggttcgatgaacc 20

RESULT 3
AA061457/C
ID AA061457 standard; DNA; 432 BP.
XX
AC AA061457;
XX
DT 17-MAY-1994 (first entry)
XX
DE *M. tuberculosis* rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PE 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
XX
PR 30-APR-1992; 92US-0875940.
XX
PR 14-AUG-1992; 92US-0929206.
XX
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
XX
PA (INSP) INST PASTEUR.
XX
PA (MEDI-) MEDICAL RES COUNCIL.
XX
PA (DYBE-) UNIV BERNE.
XX
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX Young D, Zhang Y;
XX
DR WPI: 1993-366812/46.
XX
DR P-PSDB: AAR51372.
XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
PS Example 2; Fig 13; 97pp; English.
XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium lepre strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051332) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M. tuberculosis (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag- a
FT /*note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag- b
FT /*note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (isoniazid), mbaA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), emmB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcgcttcgatgaacc 20
|||||
DB 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; Identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag- a
FT /*note= "primer of AAA49823"
FT primer_bind 372..391
FT /*tag- b
FT /*note= "primer of AAA49824"
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Hetsler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 43pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (R1M) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 296 TACGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA: 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from *Mycobacterium tuberculosis*.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KM *Staphylococcus*; Identification; detection; ds.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 296 TACGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA: 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from *Mycobacterium tuberculosis*.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KM *Staphylococcus*; Identification; detection; ds.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

Query Match	Best Local Similarity	Score 20;	DB 17;	Length 620;
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
1	tacggcgttcgatgaacc	20		
296	TACGGCGTTTCGATGACCC	277		
RESULT 8				
AAT09676/c	AAT09676/c			
ID	AAT09676 standard; DNA: 970 BP.			
AC	AAT09676;			
XX	15-OCR-1996 (first entry)			
DT	Mycobacterium tuberculosis rpoB gene DNA sequence.			
XX				
XX	Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;			
KW	polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.			
XX	Mycobacterium tuberculosis.			
OS				
XX				
FH	Key	Location/Qualifiers		
FT	primer_bind	10..27		
FT		/*tag= a		
FT		/note= "primer FENLFP"		
FT	primer_bind	226..243		
FT		/*tag= b		
FT		/note= "primer DDIDL"		
FT	primer_bind	226..240		
FT		/*tag= c		
FT		/note= "primer DDIDH"		
FT	primer_bind	338..364		
FT		/*tag= d		
FT		/note= "primer rpo95"		
FT	primer_bind	348..373		
FT		/*tag= e		
FT		/note= "primer rpo105"		
FT	primer_bind	354..373		
FT		/*tag= f		
FT		/note= "primer KY290"		
FT	misc_feature	372..373		
FT		/*tag= g		
FT		/note= "M. tuberculosis signature nucleotide"		
FT	misc_feature	433..434		
FT		/*tag= h		
FT		/note= "M. tuberculosis signature nucleotide"		
FT	misc_feature	438		
FT		/*tag= i		
FT		/note= "M. tuberculosis signature nucleotide"		
FT	misc_feature	468..469		
FT		/*tag= j		
FT		/note= "M. tuberculosis signature nucleotide"		
FT	misc_feature	486		
FT		/note= "M. tuberculosis signature nucleotide"		

Query Match	Best Local Similarity	100.0%;	Score 20;	DB 17;	Length 970;
Matches 20; Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;				

1 tacggcgttcgatgaacc 20
 |||
 671 TACGGCGTTTCGATGAACCC 652

```
RESULT 9
AAH51976/c
ID AAH51976 standard; DNA: 3519 BP.
XX
AC AAH51976;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KM Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000MO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
XX
PR 12-NOV-1999; 99US-0165124.
XX
PR 01-FEB-2000; 2000US-0179531.
XX
PA (RBC ) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM.
XX
DR WPI: 2001-329193/34.
XX
DR P-PSDB; AAG81125.
XX
XX
PT Identifying nucleotide or polypeptide sequence for use as drug target.
PT Involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure; Page 68-69; 207pp; English.
XX
XX
CC This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other:
XX
XX
Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 tacggcggttcgatgaacc 20
Db 1529 TACGGCGTTTCGATGAACCC 1510
XX
XX
RESULT 10
AAH02079/c
ID AAH02079 standard; DNA: 3534 BP.
XX
AC AAH02079;
XX
DT 24-JUL-2001 (first entry)
```

```
XX
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KM Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
XX
OS Mycobacterium tuberculosis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
XX
PR 19-MAY-2000; 2000CA-2307010.
XX
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI: 2001-245006/25.
XX
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitcal species in a test sample -
XX
PS Disclosure; Page 1478-1479; 1580pp; English.
XX
XX
CC The present invention describes a method for generating a repertory of
CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitcal
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitcal species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other:
XX
XX
Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 tacggcggttcgatgaacc 20
Db 1547 TACGGCGTTTCGATGAACCC 1528
XX
XX
RESULT 11
```

```

AAAT4651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
XX rifampin resistance; mutation detection; ds.
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
XX particularly for detecting rifampin resistance in Mycobacterium
XX tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||

```

```

PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
XX Mycobacterium, comprising detecting mutations in a gene and relating
XX them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||

```

```

RESULT 12
AAA89994/C
ID AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
XX RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX

```

```

RESULT 13
AAT12096
ID AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
XX determination; amplification; tuberculosis; rpoB; fragment;
XX primer; differential; hybridisation; pattern; rifampicin;
XX rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinx L, Portals F;

```

PI Rossau R;
 XX WPI: 1996-040250/04.
 DR
 XX
 PT Probe and primers for determ. of antibiotic resistance spectrum of
 PT Mycobacterium, opt. coupled with species identification - from
 PT different patterns of hybridisation with rpoB gene
 PS
 XX Claim 22: Page 39: 69pp: English.
 CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
 CC determined by amplifying the relevant part of the antibiotic
 CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
 CC amplified using the primer set AAT12091-98, hybridising it with at
 CC least 1 rpoB gene probe, detecting the hybrids formed and
 CC interpreting the ARS, and opt. the spp., from the differential
 CC hybridisation patterns. The method is partic. useful for the
 CC detection of rifampicin and/or rifabutin resistance in M. leprae
 CC or M. tuberculosis, and mycobacterial spp. identification. The
 CC method is rapid and reliable and provides simultaneous determ.
 CC of ARS and spp. identity.
 CC
 SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;
 OY Query Match 95.0%; Score 19; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 tacggcgcttcgatgaacc 19
 Db 1 tacggcgcttcgatgaacc 19
 RESULT 14
 ID AAO51532/C
 XX AAO51532 standard; DNA: 3447 BP.
 AC AAO51532;
 XX
 DT 17-MAY-1994 (first entry)
 XX
 DE M.leprae rpoB gene.
 XX
 KW rifampicin: antibiotic; susceptibility; sensitive; resistant; rpoB;
 KW mutant; ss.
 OS
 XX Mycobacterium leprae.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3447
 FT /*tag= "a
 FT /note= "rifampicin-sensitive; in resistant
 FT strains the Ser codon (TCG at
 FT nucleotides 1273-1275) is often mutated
 FT to a Phe, Met or esp. Leu codon"
 XX
 PN W09322454-A.
 XX
 XX
 PD 11-NOV-1993.
 PD
 PF 30-APR-1993; 93WO-EP01063.
 PF
 XX
 PR 17-SEP-1992; 92FR-0011098.
 PR 30-APR-1992; 92US-0875940.
 PR 14-AUG-1992; 92US-0929206.
 PR 16-APR-1993; 93FR-0004545.
 PR
 XX
 PA (ASSI-) ASSISTANCE PUBLIQUE.
 PA (INSP) INST PASTEUR.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PA (UYBE-) UNIV BERNE.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX
 PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
 PI Young D, Zhang Y;
 XX
 XX
 DR WPI: 1993-368812/46.
 DR P-PSDB; AAR43671.
 PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
 PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
 PT by detecting mutation in katG, rpoB or rpsL genes
 PS
 XX Example 2: Fig 12; 97pp: English.
 CC PCR amplification was used to obtain rpoB genes from rifampicin-
 CC resistant Mycobacterium leprae strains. A comparison with the
 CC sequence of the rpoB gene from sensitive strains (AAO51532) revealed
 CC mutations in the region encoding amino acids 400-450. A common
 CC mutation seen in resistant strains occurs at codon 425 where Ser is
 CC substituted, most frequently by Leu.
 CC
 SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;
 OY Query Match 92.0%; Score 18.4; DB 14; Length 3447;
 Best Local Similarity 95.0%; Pred. No. 3;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 tacggcgcttcgatgaacc 20
 Db 1454 TACGGGTGTTGATGAACCC 1435
 RESULT 15
 ID AAS51357/C
 XX AAS51357 standard; DNA: 3474 BP.
 AC AAS51357;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Enterococcus faecalis DNA for cellular proliferation protein #134.
 XX
 KW Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 OS
 XX W0200170955-A2.
 PN
 PN
 XX
 PD 27-SEP-2001.
 PD
 PF 21-MAR-2001; 2001WO-US09180.
 PF
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 PR
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PA
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 XX WPI: 2001-611495/70.
 DR P-PSDB; AAU33498.
 DR
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 XX Claim 27: Seq ID NO 3939; 51pp: English.

```

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3474 BP; 1074 A; 691 C; 776 G; 933 T; 0 other;

```

```

Query Match      84.0%; Score 16.8; DB 23; Length 3474;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 taagcgcttcgagtgaacc 20
   || ||||| ||||| ||
Db 1652 TAAGCGCTTCGATGAACC 1633

```

Search completed: August 7, 2002, 22:04:03
 Job time: 8063 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:38 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20
Sequence: 1 tacgagcttcgatgaacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

- 1: gb.ba:*
- 2: gb.htg:*
- 3: gb.in:*
- 4: gb.om:*
- 5: gb.ov:*
- 6: gb.pat:*
- 7: gb.ph:*
- 8: gb.pl:*
- 9: gb.pr:*
- 10: gb.ro:*
- 11: gb.sts:*
- 12: gb.sy:*
- 13: gb.un:*
- 14: gb.vl:*
- 15: em.da:*
- 16: em.fun:*
- 17: em.hum:*
- 18: em.in:*
- 19: em.jnu:*
- 20: em.on:*
- 21: em.or:*
- 22: em.ov:*
- 23: em.pat:*
- 24: em.ph:*
- 25: em.pl:*
- 26: em.ro:*
- 27: em.sts:*
- 28: em.un:*
- 29: em.vl:*
- 30: em.htg.hum:*
- 31: em.htg.inv:*
- 32: em.htg.other:*
- 33: em.htgo.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

C	1	20	100.0	432	1	MSGRIFFNAP	L05910	Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448	Sequence
C	3	20	100.0	620	6	AR062056	AR062056	Sequence
C	4	20	100.0	620	6	AR062057	AR062057	Sequence
C	5	20	100.0	620	6	AR062058	AR062058	Sequence
C	6	20	100.0	620	6	AR062059	AR062059	Sequence
C	7	20	100.0	620	6	AR062060	AR062060	Sequence
C	8	20	100.0	620	6	AR062061	AR062061	Sequence
C	9	20	100.0	705	1	AF060353	AF060353	Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128	Sequence
C	11	20	100.0	970	6	I50706	I50706	Sequence
C	12	20	100.0	3534	6	AX111339	AX111339	Sequence
C	13	20	100.0	3853	1	MTU12205	MTU12205	Sequence
C	14	20	100.0	5084	1	MSGRPOB	MSGRPOB	Sequence
C	15	20	100.0	19352	1	AE006964	AE006964	Mycobacte
C	16	20	100.0	19770	1	MTG1376	MTG1376	Mycobacte
C	17	18.4	92.0	626	1	AF060295	AF060295	Mycobacte
C	18	18.4	92.0	703	1	AF060349	AF060349	Mycobacte
C	19	18.4	92.0	705	1	AF060279	AF060279	Mycobacte
C	20	18.4	92.0	705	1	AF060290	AF060290	Mycobacte
C	21	18.4	92.0	705	1	AF060293	AF060293	Mycobacte
C	22	18.4	92.0	705	1	AF060297	AF060297	Mycobacte
C	23	18.4	92.0	705	1	AF060299	AF060299	Mycobacte
C	24	18.4	92.0	705	1	AF060300	AF060300	Mycobacte
C	25	18.4	92.0	705	1	AF060325	AF060325	Mycobacte
C	26	18.4	92.0	705	1	AF060326	AF060326	Mycobacte
C	27	18.4	92.0	705	1	AF060327	AF060327	Mycobacte
C	28	18.4	92.0	705	1	AF060328	AF060328	Mycobacte
C	29	18.4	92.0	705	1	AF060329	AF060329	Mycobacte
C	30	18.4	92.0	705	1	AF060331	AF060331	Mycobacte
C	31	18.4	92.0	705	1	AF060351	AF060351	Mycobacte
C	32	18.4	92.0	705	1	AF060366	AF060366	Mycobacte
C	33	18.4	92.0	3316	1	AF172323	AF172323	Bacillus
C	34	18.4	92.0	3447	6	AR067447	AR067447	Sequence
C	35	18.4	92.0	37617	1	MLB1790G	MLB1790G	Sequence
C	36	18.4	92.0	348950	1	MLEPRTN7	MLEPRTN7	Sequence
C	37	17.4	87.0	10909	1	AE007977	AE007977	Agrobacte
C	38	17.4	87.0	13047	1	AE009010	AE009010	Agrobacte
C	39	16.8	84.0	518	1	AF325874	AF325874	Staphyloc
C	40	16.8	84.0	643	1	AF060346	AF060346	Mycobacte
C	41	16.8	84.0	647	1	AF060350	AF060350	Mycobacte
C	42	16.8	84.0	652	1	AF060344	AF060344	Mycobacte
C	43	16.8	84.0	652	1	AF060364	AF060364	Mycobacte
C	44	16.8	84.0	705	1	AF060283	AF060283	Mycobacte
C	45	16.8	84.0	705	1	AF060285	AF060285	Mycobacte

ALIGNMENTS

RESULT 1
MSGRIFFNAP/c 432 bp DNA linear BCT 21-MAY-1993
LOCUS Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
DEFINITION resistance gene, complete cds.
ACCESSION L05910.1 GI:149991
VERSION RNA polymerase beta-subunit; rifampicin resistance.
KEYWORDS Mycobacterium tuberculosis (strain H37) DNA.
SOURCE Mycobacterium tuberculosis
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 432)
REFERENCE
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES
Location/Qualifiers
1..432
/organism="Mycobacterium tuberculosis"
/strain="H37"

CDS

/db_xref="taxon:1773"
 <1..>432
 /codon_start=1
 /transl_table=11
 /product="RNA polymerase beta subunit"
 /protein_id="AAB59068.1"
 /db_xref="GI:149992"
 /translation="GNRLRTVGGELIONQIRVGSRMERYRMTTODVEATPPTL
 IIRPVAAIKKEFGTSOLSDPMDNNLSGLTHKRRRLSALGPGSLSRKAGLEVRD
 HPSHYGRMCPIETEPGPNGLGLSLVARKVPEGFETPYR"
 149

variation
 /phenotype="rifampicin resistant in association with
 mutation 234 G"
 /replace="C"
 188

variation
 /phenotype="rifampicin resistant"
 /replace="C"
 191

variation
 /phenotype="rifampicin resistant in association with
 mutation 203 T"
 /replace="C"
 194

variation
 /phenotype="rifampicin resistant"
 /replace="T"
 203

variation
 /phenotype="rifampicin resistant"
 /replace="T"
 208..210

variation
 /phenotype="rifampicin resistant"
 /replace=""
 232

variation
 /phenotype="rifampicin resistant"
 /replace="G"
 232

variation
 /phenotype="rifampicin resistant"
 /replace="a"
 233

variation
 /phenotype="rifampicin resistant"
 /replace="g"
 233

variation
 /phenotype="rifampicin resistant"
 /replace="g"
 233

variation
 /phenotype="rifampicin resistant"
 /replace="C"
 234

variation
 /phenotype="rifampicin resistant"
 /replace="g"
 247..248

variation
 /phenotype="rifampicin resistant"
 /replace="Ca"
 248

variation
 /phenotype="rifampicin resistant"
 /replace="g"
 248

variation
 /phenotype="rifampicin resistant"
 /replace="T"
 254

variation
 /phenotype="rifampicin resistant"
 /replace="C"
 254

BASE COUNT 77 a 140 c 148 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
 |||
 DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
 AR067448/c 432 bp DNA linear PAT 29-SEP-1999
 LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
 ACCESSION AR067448
 VERSION AR067448.1 GI:5998670
 KEYWORDS
 SOURCE
 ORGANISM
 UNKNOWN.
 REFERENCE
 AUTHORS
 1 (bases 1 to 432)
 Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
 Bomer, T.
 TITLE
 Rapid detection of antibiotic resistance in mycobacterium
 tuberculosis
 JOURNAL
 Patent: US 5851763-A 59 22-DEC-1998;
 FEATURES
 location/Qualifiers
 source
 1..432
 /organism="unknown"
 BASE COUNT 77 a 139 c 149 g 67 t

Query Match 100.0%; Score 20; DB 6; Length 432;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
 |||
 DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
 AR062056/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062056
 DEFINITION Sequence 135 from patent US 5843669.
 ACCESSION AR062056
 VERSION AR062056.1 GI:5989747
 KEYWORDS
 UNKNOWN.
 ORGANISM
 UNKNOWN.
 REFERENCE
 1 (bases 1 to 620)
 AUTHORS
 Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
 TITLE
 Cleavage of nucleic acid using thermostable methanococcus
 jannaschii FEN-1 endonucleases
 JOURNAL
 Patent: US 5843669-A 135 01-DEC-1998;
 FEATURES
 location/Qualifiers
 source
 1..620
 /organism="unknown"
 BASE COUNT 103 a 202 c 214 g 101 t

Query Match 100.0%; Score 20; DB 6; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
 |||
 DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
 AR062057/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062057
 DEFINITION Sequence 136 from patent US 5843669.
 ACCESSION AR062057
 VERSION AR062057.1 GI:5989748
 KEYWORDS
 UNKNOWN.
 ORGANISM
 UNKNOWN.
 REFERENCE
 1 (bases 1 to 620)
 AUTHORS
 Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
 TITLE
 Cleavage of nucleic acid using thermostable methanococcus

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 137 from patent US 5843669.
DEFINITION AR062058
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 138 from patent US 5843669.
DEFINITION AR062059
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 139 from patent US 5843669.
DEFINITION AR062060
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 140 from patent US 5843669.
DEFINITION AR062061
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene.
DEFINITION

partial cds.
AF060353
AF060353.1 GI:313464
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 705)
AUTHORS
Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M.,
Drobniawski, F., Alland, D., Desmond, E., Holodny, M., and Drenkow, J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
JOURNAL
Genome Res. 8 (5), 435-448 (1998)
MEDLINE
98248685
REFERENCE
2 (bases 1 to 705)
AUTHORS
Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M.,
Drobniawski, F., Alland, D., Desmond, E., Holodny, M., and Drenkow, J.
Direct Submission
JOURNAL
Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
source
1..705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:1773"
<1..>705
/gene="rpoB"
/gene="rpoB"
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AAC38533.1"
/db_xref="GI:313465"
/translation="QDEAITPQTLINIRPVVAIKFEFTSOLQPMQDNPLSGLT
HKRRLSALGGSLSRERAGLEVSRGSGRCPTEPGNIGLSVYARVP
EGFETPYRVGVGVSDEIVLTADDEHHVVAQANSPIDACGRPEPVLYRRKRG
EVEYPSSEVDYNDVSPROMVSATAMIPLEHDDNRALMGANMORQAVPLVSEAP
LVGTGMELRALIDAT"

BASE COUNT 117 a 227 c 250 g 111 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 331 TACGGCGTTTCGATGAACCC 312

RESULT 10
ARI49128 706 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION
Sequence 24 from patent US 6228575.
ARI49128
ACCESSION
ARI49128.1 GI:15113719
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 706)
AUTHORS
Gingeras, T.R., Mack, D., Chee, M.S., Berno, A.J., Stryer, L.,
Ghandour, G., and Wang, C.
Chip-based species identification and phenotypic characterization
of microorganisms
Patent: US 6228575-A 24 08-MAY-2001;
JOURNAL
Location/Qualifiers

source 1..706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313

RESULT 11
150706/c 970 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION
Sequence 1 from patent US 5643723.
150706
ACCESSION
150706.1 GI:2472409
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 970)
AUTHORS
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmler, T.A., Roberts, G.D.
and Whelan, A. Christian.
Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
JOURNAL
Location/Qualifiers
FEATURES
source
1..970
/organism="unknown"
BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
AX111339 3534 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION
Sequence 2072 from Patent WO0123604.
AX111339
ACCESSION
AX111339.1 GI:13927631
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
AUTHORS
Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J., and Roy, P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
JOURNAL
Infectio Diagnostic (I.D.I.) INC. (CA)
TITLE
Location/Qualifiers
FEATURES
source
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 1547 TACGGCGTTTCGATGAACCC 1528

RESULT 13
MTU12205/c 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE
ORGANISM

Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.

TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 3853)
Imboden, P.
REFERENCE Direct Submission
JOURNAL Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland

FEATURES
source location/Qualifiers

1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
576..>3853
/gene="rpoB"
/codon_start=1
/transl_table=1
/product="RNA-polymerase beta subunit"
/protein_id="AAA20242.2"
/db_xref="GI:7144499"

/translation="MLEGCTIADRSKTAASPSRPOSSNNNSVPGANRVSAFL
REPLEVGLDVOTDSFEMLTGSFRMRSAERKDVNPVGLSEVLYELSPEDFSS
MSLSFSDPRDDVKAPEDECKDMTYAAPLEVAEPIINNTEIKSQTFMGDFPM
TEKGTFLINTEKRRPVVQLVSPGVYEDETIDKSTDLHSVKVPSRGAMLEFVDK
RDYGVGIDRRKRPVTVLLKALGMTSEQIVERRGSEIMRSTLEKNTVGTDEALD
IYKRLRGEPTKESAOITLENFEKRYDLARVGRYKVKKLGHLVGPITSTLT
EEDVATITELVRLHESQTTMTPVGVGVPEVETDDIDHFGRRRLRTYGELOQIRVG
MSRMERYRERMTTQDVEAITPOTLINIRPVAAIKFEGTSQLSQPMONNPISGLT
HKRRLSALGPGSLSERAGLEVHVHPSHRGRCPIETPEGPNGILGSLSVARVNP
FGFLETPYRKVVGVSDGIVYLADDEDRHVVAQNSPIDADGRFEPRLVARRKAG
EVEVYPSSEVDVMPROMVSVATAMIPELEHDARALGAMORAOAVLVRSKAG
LVNGGMLRAIDAATSSQSGVIEEVSADYITVMHNGTRRTYRMKRFARSNHGC
ANOCPIYADGRVAGOVYADGPTDGEALGNLVAIMPMEGHYEDAILSNL
VEEDVLSITHIEHEDARDTKLGAETITRDIPNISDEVLADDERGIVIRGAERVKG
DILVGVTPKGETELTPEERLRAIFEGKAREVNDISLKVPHGESGVIGIRFESRD
EDELPAVNLVRYVVAOKRISDGRLAGHNGKVGIGKILPVEDMPLADGPVYDI
ILNTHGVRNNIGLOILETHLGMCAHSGMKVDAKGVDMARLPDELLEHANAIVS
TPVEDGAOEALGLOLSCITLPNRGDVLYVADGKAMLPDGRSGEPFYPVYGVYIM
KLHLVYDVKIHAIRSTGYSMITQOPLGSKAOFGGRGEMECAMQAVGAAYTIQELL
TIKS"

BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 14
MSGRPOB 5084 bp DNA linear BCT 13-SEP-1994
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
DEFINITION gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
partial cds.
ACCESSION L27989.1 GI:468333
VERSION L27989.1
KEYWORDS RNA polymerase beta-subunit; rpoB gene.
SOURCE Mycobacterium tuberculosis (strain Rv) DNA.
ORGANISM

Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 5084)
Miller, L.P., Crawford, J.T. and Shinnick, T.M.

TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
MEDLINE 94304130
FEATURES location/Qualifiers

1..5084
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
1065..4598
/gene="rpoB"
1065..4598
/gene="rpoB"
/codon_start=1
/transl_table=1
/evidence=experimental
/product="RNA polymerase beta-subunit"
/protein_id="AAA21416.1"
/db_xref="GI:468334"

/translation="MLEGCTIADRSKTAASPSRPOSSNNNSVPGANRVSAFL
REPLEVGLDVOTDSFEMLTGSFRMRSAERKDVNPVGLSEVLYELSPEDFSS
MSLSFSDPRDDVKAPEDECKDMTYAAPLEVAEPIINNTEIKSQTFMGDFPM
TEKGTFLINTEKRRPVVQLVSPGVYEDETIDKSTDLHSVKVPSRGAMLEFVDK
RDYGVGIDRRKRPVTVLLKALGMTSEQIVERRGSEIMRSTLEKNTVGTDEALD
IYKRLRGEPTKESAOITLENFEKRYDLARVGRYKVKKLGHLVGPITSTLT
EEDVATITELVRLHESQTTMTPVGVGVPEVETDDIDHFGRRRLRTYGELOQIRVG
MSRMERYRERMTTQDVEAITPOTLINIRPVAAIKFEGTSQLSQPMONNPISGLT
HKRRLSALGPGSLSERAGLEVHVHPSHRGRCPIETPEGPNGILGSLSVARVNP
FGFLETPYRKVVGVSDGIVYLADDEDRHVVAQNSPIDADGRFEPRLVARRKAG
EVEVYPSSEVDVMPROMVSVATAMIPELEHDARALGAMORAOAVLVRSKAG
LVNGGMLRAIDAATSSQSGVIEEVSADYITVMHNGTRRTYRMKRFARSNHGC
ANOCPIYADGRVAGOVYADGPTDGEALGNLVAIMPMEGHYEDAILSNL
VEEDVLSITHIEHEDARDTKLGAETITRDIPNISDEVLADDERGIVIRGAERVKG
DILVGVTPKGETELTPEERLRAIFEGKAREVNDISLKVPHGESGVIGIRFESRD
EDELPAVNLVRYVVAOKRISDGRLAGHNGKVGIGKILPVEDMPLADGPVYDI
ILNTHGVRNNIGLOILETHLGMCAHSGMKVDAKGVDMARLPDELLEHANAIVS
TPVEDGAOEALGLOLSCITLPNRGDVLYVADGKAMLPDGRSGEPFYPVYGVYIM
KLHLVYDVKIHAIRSTGYSMITQOPLGSKAOFGGRGEMECAMQAVGAAYTIQELL
TIKSDDVLRKAVVETALVKGNIPEPGIPESFKVLKLELOSLCLNVEVLSDDGAIEL
REGDEDLERVAANMIGILSNESASFEDLA"

gene 4641..5084
/gene="rpoC"
4641..>5084
/gene="rpoC"
/codon_start=1
/transl_table=1
/product="RNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:537608"

```

/translation="MDVNFPEDELRLGLAADIROMSYGEVKKPEIINRITLKPEED
GLPCEKITEPTDMECYCGKYKRVRFKGIICERCYGVTAQKVRREMGHIELAPVT
HIMFKGVPSRLGLLDLAPKDEKIIYFAAYITVSDEERHNEL"
BASE COUNT      969 a      1534 c      1691 g      890 t
ORIGIN

```

Query Match	100.0%	Score 20	DB 1	Length 5084
Best Local Similarity	100.0%	Pred. No. 2.1		
Matches 20	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

QY      1  tacgycgttcgatgaacc 20
          |||
Db      2611 TACGGCGTTTCGATGAACCC 2592

```

RESULT	15		
AE006964/C			
LOCUS		19352 bp	DNA
DEFINITION	AE006964		linear BCT 27-APR-2001
	Mycobacterium tuberculosis CDC151,	section 50 of 260 of the	

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AE006964 AE000516 AE006964.1 GI:13880217	Mycobacterium tuberculosis CDC151. Mycobacterium tuberculosis CDC151.

REFERENCE	AUTHORS
1 (bases 1 to 19352)	Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,

TITLE Whole genome comparison of *Mycobacterium tuberculosis* clinical and laboratory strains
JOURNAL Unpublished

JOURNAL
 REFERENCE
 AUTHORS
 Unpublished
 2 (bases 1 to 19352)
 Flutschmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
 Peterson,J., Deboy,R., Dodson,R., Gwin,M., Hart,D., Hickey,E.,
 Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermoaleva,M.,
 Salzberg,S.L., Delcher,A., Uterback,T., Weidman,J., Khouri,H.,
 Gill,J., Mikula,A. and Bishai,W.
 TITLE
 JOURNAL
 Direct Submission
 Submitted (25-APR-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA

source	1. .19352
--------	-----------

```
gene 163..3699
      /gene="MT0695"
CDS 163..3699
```

```

/gene="A10935
/note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
PFI:D49992; identified by sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK4921.1"
/db_xref="GI:13880218"

```

REPLEVPGLLQVNDHFEFJMLXSPMRKRAAPRQEDVNVFCGLEVEILVELSPJEDDSF
MLESJSDRPFDVDAVBECKDKDMTYSAPLPAFVAEEFNNTGKEKSLQYMGDFPMAR
TEKGFEJINGTERVNVSVOLVSXPGYVEFEDTDEKSTDKLSVKYKIPSGALAEEDVAD
RDYVGRJEDRRORPQVVLKALCMSTSOIYERGFSEIMSTJELKNDVGTGTDALDLD
IYRKIRPEGPETKESAOJLTLENLFEFKERYKQPLAVAGRYKVRKJGLANGHEJTSSTL
EDVAVATEPYVLHGEQJMTNVGVCVEVPEJDIHQFNRKJGKJLQVTEJLQNIORVQ
MSRMRVYREHMTQODVAIRPQJLINTRPVMAIKKEFFQNSQJOFENDOMJLGSJLT
HKRRVYALGPGLSRERAGJLEVPDVRHSHRYVMAIEPEEPGPNJLQJGSSJLTVYRVND

```
gene      3744. 7694  
          /gene="MT0696"  
CDS      3744. 7694  
          /CDS="ATGACGCGG
```

```

/note="similar to SP:P37871; identified by sequence
similarity: putative"
/codon_start=1
/transl_table=11
/product="DNA-directed RNA polymerase, beta-prime subunit"
/protein_id="AAK492.1"
/db_xref="GI:13880219"

```

/translition="MUDVNFDEBLRIGLATEEDRMSYSGVKKPEKINRTKLPEAD
 GJCEKJEPIDMECCYCGKYKRRVFRGITECGRGVYTRAKVREMGHLELTAAP
 HIWYKQPSRKLGLLDAPKOLEKIIYFAAYVITSYDEBNRHNELSTLEABAVERK
 AVEEDRDELEBARQKLEADLELBAEACDARKKRDGSEMRORI RORACELD
 LVEDDSTLELAPOLIVDENLYRELDVRCYETPGAMGESIOKLENDIDAEAS
 LEDYTRNKGCGKLTALRKLTVAAFOOSGSPMGVNLDAVPELRLPMVQJIDGGR
 FATSJLRYRVIRINBNRLKRIDLAPETIYNNKMRMOESVDLAFDNGRCRPAT

GPGNRPKLSLSDLKGKRGKRNVLNKGKRVSGSRVLYVSPOLKIHQGLPKPTLMALG
 LEKPPVKNRLVDLNLNAPQKRSKRNKREKORPQVADLBEVYLAEPVLLNNRPLTHRIG
 IQAFPPMLVEKKAIOIAPHLVCEAFNAQDFGQWVHLPLSEAEQAEKRIITLMSNNLT
 SPASRPPAMPBRLDMVETGLVYLTTEVEPDETCQSPAGSDHETTVSGSPMELIAMAOR
 GLVSRALIKTVRLDOLRPVELEAELEFCHSGMGQDMMKETTGLGRVPMELLPLGYP
 EYNNKMHKKVQAAIITNDLAERYYPVIAVQAOTDKLDGFGVATSSGTVSADIVLPP
 EYKRTIDHKKVQAAIITNDLAERYYPVIAVQAOTDKLDGFGVATSSGTVSADIVLPP

TANKLELDH EENAADEVEQUTORGANINBERKEKEDTET
 ITTIVDSASTGETFOTRTI LAGMKGLVITNKEKEDTETPRV KSSFRGGLVLEFIINTHBA
 RGLAGDILRTIADSGEITLRRLAVDYSODIYAEHPCOCITGLVLELAPARSLVLCALITSD
 YLETSIAVTRITGTDPAVDEAGNIVERGDDILADPEIDLALAGITVAVRSLVILCAITSD
 GCAICVCRSMATKILADVITGEAVRIVAAOSIGEGEOTITRITFQVSGEVDKETITGLER
 VOELCEAVRPGKRAILADVITGRVLEDEBERYKITTIVDDGGEETVAVDKITSKRORLIV
 KHEDGSEVITSDGHDHVEVGOQLMEGSDAPHEIVLRVGOVPRVQHLVRAVEQVYRRAAG
 VSIHOKHTEIVTRVLOMRLRVRTIIDSGETEFLGSDILDRNEFAENKRVVAVAGGGEPAAR

gene
CDS

```
PLMRLITATASATDSMTLSAASFOETTRRLTDLAAINCSDSKLNGLKENVIIGKILIPACT
G1NPG1N1AVOPEETEEAARAAYTIPSEDOYSSPDGAATGAAYPLDDYGYSDVR"
complement(7691.. .8065)
/gene="MT06597"
complement(7691.. .8065)
/gene="MT0697"
/note="identified by Glimmer2; putative"
```

```

/codon_start=1
/codon_table=11
/product="hypothetical protein"
/protein_id="AAK4923.1"
/db_xref="GI:13880220"
/translation="MFDSSAAAITNPGHAMASAMERSGCLIECVAGLDEPGFEAFADKL
NDSSSSRRVPRQADGSIATHVVERGGSGRSGGAGVPPRMGPALAMODLIHH

```

gene
GEOITONRIAGAEFRVRECYCSPT"
complement(8056. .9972)
/gene="MT0698"
/note="This region contains an authentic frame shift and
is not the result of a sequencing artifact. Identified by
Glimmer2; putative, conserved hypothetical protein.

gene	accession	description
CDS	10167.10925	authentic frameshift
	/gene="MT0699"	
	10167.10925	
	/gene="MT0699"	
	/note="identified by match to PFAM protein family HMM PF01261"	

```
/codon_start=1
/transl_table=11
```

/product="Ap endonuclease, family 2"
/protein_id="AAK44924.1"
/db_xref="GI:13880221"
/translation="MLIGSHVSPTDPLAAAEAGADVQVIFLGPQSKAKRPDDAA
ALKATLPTVHAFYLLINLASANNRVRIPSKLIQETCAADIGAAAVYHGSHVAD
DNIDKGFQRMRLDLRLLETVPVYLENTAGDAMARREPTILADVIDGTIGIC
LDVCHTWAGAEALTDADRIKAITGRIDLVCHNSRDEAGSGRDRHNLGSGQIDPDL
LVAAVKAAGAPVICETADQGRKDIAFLRERTGS"
10957.11799
/gene="MT0700"
10957.11799
/gene="MT0700"
/note="similar to GB:U00012 PID:46863; identified by
sequence similarity; putative"
/codon_start=1
/transl_table=1
/product="hydrolase/esterase, putative"
/protein_id="AAK44925.1"
/db_xref="GI:13880222"
/translation="MLRVAITLAAVLAFAAGCGGTRLAAGFGNGNSVHTLDVAGR
SYRLKRPVGLPSSAPLVVMLHGSGAKAERSGMEIADSEKELVAYPDGHRAN
ANGGCCGRRPAREVDIGFRAVYADIANNVSIDPARVYTGMSNGHINSYTLACNT
SIFAIQVSGTQDPCQSPRVSIVIHGTADPLVRIHGGPGAGFARIDGPVPDDL
AFWREVNRCGALDITTEGVPVTSATCADNRVYLLTVDAHRMPSFATQTLWFFA
AHFR"
11859.13487
/gene="MT0701"
11859.13487
/gene="MT0701"
/note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
putative"
/codon_start=1
/transl_table=1
/product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK44926.1"
/db_xref="GI:13880223"
/translation="MSDTHVVTNOVPLENYPASSPYLIEALIOEGGOMGLDEVNEV
GATASCOAORWGLADNRPIILHTDAVGYRDEVEDEPAVHELMRATHGMAAP
WADRRPAHYRAKTSWYTERGHICPISMTYAVVPALRYNSELAAYEPLTSREY
DPELKPATYKAGITAGMSWTEKQGSQDVRACTQATPADGSYSLTGKWFSAQCD
IFVLAQAPDGLSCFLPRVLPDGRNRMFLQRLDKLGNHANSSEVEYDGAVALV
GEEGRGVPTTIENYLTDLCLGSAATSMGTGLRAVHAQRAFGAYLIDPLMRN
VLADLVEAEATIVAMRAGATDNAAVGNETEARLRRIGLAAKAYWCKRSTAAAE
ALECLGNGYVEDSGMRLYREARLGMWESGVSALDTIRAMATPRACYEVLDEL
ARSAQDPRLDGHEVRLPQIGLDLTIGTRARKTAEDICLALQSSLLVRHGHPAAEA
FLATRLGGOWGCAITMPAGIDLPIERALVKG"
13498.14436
/gene="MT0702"
13498.14436
/gene="MT0702"
/note="similar to GP:3885480; identified by sequence
similarity; putative"
/codon_start=1
/transl_table=1
/product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK44927.1"
/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKTMTYEVTGRIARTTFNRPEKNAIADTPL
ELSLVSRADLDPGVHVILVSGREGFCAGFDLSAEGSSSTGGGAYOGTVLDGKT
QAVNHLNPNQPMIDYOMSRFVRFGLSMHADKPTVVKIHGYCVAGGTDIALHADQ
VIAADAKIGYPTFRVWGVPRAAGLMAHRIGDRAKRLLEFTGDCITGAQAAMEGLAVEA
PEPADDERTERLVARITAPVNOILINKLALNSALLDQGVATSRMSTVYFDGAARRT
PEGHAFVADAVEHGFDAVRRRDEPFGDYGQASRV"
14439.15161
/gene="MT0703"
14439.15161
/gene="MT0703"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"

Query Match 100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcgttcgataaaccc 20
|||||
DB 1709 TACGGCGTTTCGATGAACCC 1690

Search completed: August 7, 2002, 21:51:46
Job time: 23881 sec

Matches	19, Conservative	0, Mismatches	1, Indels	0, Gaps
Qy	1	tacggtcggcgagctgattcc	20	
Db	94	TACCGTCGGCGGAGCTGATCC	75	

RESULT	2
BM396091/c	
LOCUS	132 bp mRNA
DEFINITION	5009-0-17-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)

ORGANISM	<i>Tetrahymena thermophila</i>
ETIMATOLOGY	Eutaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE	1 (bases 1 to 132)
AUTHORS	Turkewitz, A. P., Karrer, K. M., Jahn, C., Orlas, E., Kirk, K. E., Frankel, J., and Klobutcher, L.
TITLE	EST from <i>Tetrahymena thermophila</i> , strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP

920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurturkew@midway.uchicago.edu

FEATURES	source	Location/Qualifiers
1..132		
		/organism="Tetrahymena thermophila"
		/strain="CU428.1"
		/db_xref="taxon:5911"
		/clone_idb="Chlcoat/Turkewitz cDNA (large fraction)"
		/note="Vector: Bluescriptp2 SK+, details on library preparation can be found in Chlcoat and Turkewitz (2001) Proc. Natl. Acad. Sci. USA, 98: 8709-8713."
BASE COUNT	27 a	42 c
ORIGIN		44 g
		19 t

Query Match	92.0%	Score 18.4	DB 10	length 132
Best Local Similarity	95.0%	Pred. No. 1.7e+02		
Matches 19	Conservative	0	Mismatches 1	Indels 0
0Y	1	tacgtctcgagcagctcgatcc	20	
Db	96	TACCGTCGCGCAGCTGCATCC	77	

RESULT	3	134	bp	linear	EST	17-JAN-2002
BM398255/c						
LOCUS	BM398255					
DEFINITION	5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)					
	Tetrahymena thermophila cDNA, mRNA sequence.					

KEYWORDS EST. *Tetrahymena thermophila*.
SOURCE *Tetrahymena thermophila*.
ORGANISM Eukaryota; Alveolata; Ciliophora; Olisophenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

BASE COUNT	26 a	44 c	46 g	18 t
ORIGIN				

Query Match	92.08%	Score 18.4	DB 10	Length 134
Best Local Similarity	95.08%	Pred. No. 1.7e+02		
Matches 12	Conservative	0	Mismatches 1	Indels 0
Gaps 0				
QY	1	tacggtcgagcagctgtatcc	20	
Db	98	TACCGTCGCGAGCGATGCC	79	

RESULT	4
CNS01GJZ/c	
LOCUS	984 bp
DEFINITION	DNA linear GSS 01-JUN-2001
	Anopheles gambiae GSS T7 end of clone 06016 of NotreDame1 library
	from strain PEST of Anopheles gambiae (African malaria mosquito),
	genomic survey sequence.

ORGANISM Anophelinae: Anopheles gambiae; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 984)

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
2 (bases 1 to 984)	Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.	Direct submision	Submitted (16-FEB-2000) BBMT, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

BASE COUNT	272 a	236 c	241 g	232 t	3 others
ORIGIN					

Query Match	87.0%;	Score 17.4;	DB 12;	Length 984;
Best Local Similarity	94.7%;	Pred. No. 7.4e+02;		
Matches 18; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Oy 1 taaggctcgagcgtatcc 19
|||||
Db 103 TACGGTCGCGAGCTAATC 85

RESULT 5
BE443802 422 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_B06.C122S wheat etiolated seedling root normalized CDNA
DEFINITION library Triticum aestivum CDNA clone WHE1132_B06.C12, mRNA
sequence.

ACCESSION BE443802
VERSION BE443802
KEYWORDS GI:9443341
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 422)

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES

Location/Qualifiers

1..422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_B06.C12"
/clone_1lb="Wheat etiolated seedling root normalized CDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pbluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pbluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 ggtcgagcgtatcc 20
|||||

Db 86 GGTGCGGAGCTGATCC 102

RESULT 6
BE445100

LOCUS WHE1132_H08.P162S wheat etiolated seedling root normalized CDNA
DEFINITION library Triticum aestivum CDNA clone WHE1132_H08.P16, mRNA
sequence.

ACCESSION BE445100
VERSION BE445100
KEYWORDS GI:9444655
SOURCE EST.
ORGANISM bread wheat.
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 544)

REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.

FEATURES

Location/Qualifiers

1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08.P16"
/clone_1lb="Wheat etiolated seedling root normalized CDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pbluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pbluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
4 ggtcgagcgtatcc 20
|||||

RESULT 7
BE444713
LOCUS
DEFINITION BE444713 558 bp mRNA linear EST 25-JUL-2000
WHE1137_H03_005Zs Wheat etiolated seedling root normalized cDNA
library Trilicium aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713 GI:9444264
VERSION BE444713
KEYWORDS EST
SOURCE bread wheat.
ORGANISM Trilicium aestivum
REFERENCE Trilicium aestivum; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Trilicium.
1 (bases 1 to 558)
Anderson, O.D., Cho, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: andersen@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..558
/organism="Trilicium aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN
Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgcgcagcctgcatcc 20
|||||
DB 514 ggtcgcgcagcctgcatcc 530

RESULT 8

BE195103
LOCUS
DEFINITION BE195103 610 bp mRNA linear EST 22-OCT-2001
HVSMEN0088E21f Hordeum vulgare 5-45 DAP spike EST library
mRNA sequence.
ACCESSION BE195103
VERSION BE195103
KEYWORDS EST
SOURCE barley.
ORGANISM Hordeum vulgare
REFERENCE Hordeum vulgare; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Hordeum.
1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.
JOURNAL Contact: Wing RA
COMMENT Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 238
Seq primer: AATTACCCCTCAGTAAGG
High quality sequence stop: 563.
Location/Qualifiers
1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEN0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCDNA009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/g99pages/dgn/31/cover.html)"

BASE COUNT 127 a 203 c 158 g 120 t
ORIGIN
Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgcagctgattcc 20
 ||||||||||||||||
 Db 499 ggtcgcgcagctgattcc 515

RESULT 9
 BE442518 658 bp mRNA linear EST 25-JUL-2000
 LOCUS WHE1101.H10.O19S wheat etiolated seedling root normalized cDNA
 DEFINITION library Trilicium aestivum cDNA clone WHE1101.H10.O19, mRNA

ACCESSION BE442518
 VERSION BE442518
 KEYWORDS EST
 SOURCE bread wheat
 ORGANISM Trilicium aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triliceae; Trilicium.
 1 (bases 1 to 658)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

JOURNAL Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

EMAIL: oanderson@wv.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stralagene SK primer.
 Location/Qualifiers

FEATURES

source
 1. 658
 /organism="Trilicium aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1101.H10.O19"
 /clone_lib="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluescript SK; Site_1: EcoRI; Site_2: XhoI. Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluescript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 144 a 203 c 165 g 140 t

ORIGIN

Query Match 85.0%: Score 17: DB 10: Length 658;
 Best Local Similarity 100.0%: Pred. NO. 1e+03;
 Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
 OY 4 ggtcgcgcagctgattcc 20

Db 512 ggtcgcgcagctgattcc 528
 ||||||||||||||||

RESULT 10
 BG299722 828 bp mRNA linear EST 17-OCT-2001
 LOCUS HVSMEa0021120f Hordeum vulgare seedling shoot EST library
 DEFINITION HVCdNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
 mRNA sequence.

ACCESSION BG299722
 VERSION BG299722
 KEYWORDS EST
 SOURCE barley.
 ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triliceae; Hordeum.
 1 (bases 1 to 828)
 Wing, R., Close, T.J., Kleinbofs, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
 Fenton, R.D. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library

JOURNAL Unpublished (2001)
 Contact: Wing R
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293

EMAIL: rwing@clemson.edu
 Total hg bases - 574
 Seq primer: AATTAACCCCTCACTAAGCG
 High quality sequence stop: 643.
 Location/Qualifiers

FEATURES

source
 1. 828
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEa0021120f"
 /clone_lib="Hordeum vulgare seedling shoot EST library
 HVCdNA0001 (COLD stress)"
 /tissue_type="Seedling shoot"
 /lab_host="TJc121"
 /note="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give pluescript SK(-) cDNA
 phagemids. These steps were performed in the TJ Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinbofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t

ORIGIN

Query Match 85.0%: Score 17; DB 10; Length 828;
Best Local Similarity 100.0%: Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgagcagctgaccc 20
|||||
Db 500 GGTGCGCAGCTGATCC 516

RESULT 11
BI188703/c
LOCUS

DEFINITION BI188703 419 bp mRNA linear EST 10-JUL-2001
d2e05fs.r1 Fusarium sporotrichioides Tti 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
sequence.

ACCESSION BI188703 GI:14662382
VERSION BI188703
KEYWORDS
SOURCE
ORGANISM Fusarium sporotrichioides.
Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 419)
Ren,Q., Tag,A., Peplow,A., Lal,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other_ESTs: d2e05fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Biotechnology
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
73 2.2 g117799258|emb|CAB90 (AL355752) putative integral
membrane protease
Seq primer: T3
High quality sequence stop: 107.
location/Qualifiers
1..419
/organism="Fusarium sporotrichioides"
/strain="Tti 10"
/db_xref="taxon:5514"
/clone_id="d2e05fs"
/clone_lib="Fusarium sporotrichioides Tti 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 117 a 106 c 117 g 79 t
ORIGIN

Query Match 84.0%: Score 16.8; DB 10; Length 419;
Best Local Similarity 90.0%: Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgaccc 20
|||||
Db 114 TACGCTGCGCAGCTGATCC 95

RESULT 12
BI1981973
LOCUS

DEFINITION BI1981973 606 bp mRNA linear EST 24-OCT-2001
f533f08.y1 zebrafish adult brain Danio rerio cDNA 5333151 5'
similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ; , mRNA sequence.

ACCESSION BI1981973
VERSION BI1981973.1 GI:16371108
KEYWORDS
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 606)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shu,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTs: f533f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
cDNA Library Preparation: John Ngai, cDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ResourcenzentrumPrimaDatenbank, Berlin, Germany (web address:
www.rzp.de)
High quality sequence stop: 446.
location/Qualifiers
1..606
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_id="5333151"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/note="Vector: pZiPlox; Site.1: NotI; Site.2: SalI;
Original library was constructed in lambdaZiPlox. Mass
excision of the cDNA library was performed to yield
pZiPlox plasmids. Insert check was done in original
library."
BASE COUNT 209 a 133 c 139 g 125 t
ORIGIN

Query Match 84.0%: Score 16.8; DB 10; Length 606;
Best Local Similarity 90.0%: Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgaccc 20
|||||
Db 452 TACGCTGCGCAGCTGTTC 433

RESULT 13
BI1888442/c
LOCUS

DEFINITION BI1888442 640 bp mRNA linear EST 12-OCT-2001
Z6537-2-000197 zebrafish shield stage whole embryo cDNA library
MPMGp637 Danio rerio cDNA clone MPMGP637_18E17;MPMGp637E17 5',
mRNA sequence.
ACCESSION BI1888442 GI:16095713
VERSION BI1888442
KEYWORDS
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 640)
Clark, M., Amstad, P., Hennig, S., Johnson, S. L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
JOURNAL
COMMENT
Contact: Hennig S
Laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innesstr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.
FEATURES
source
1..640
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMP637_18E17:MPMP637E1718"
/clone_11b="Zebrafish shield stage whole embryo cDNA
library MPMP637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 Blue MR"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
BASE COUNT
209 a 152 c 139 g 139 t 1 others
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 640;
Best Local Similarity 90.0%; Pred. NO. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 taaggtcgagcagctgaccc 20
|||||
Db 541 TAGGTCGGCGAGCTGTAC 522
RESULT 14
AM502654 292 bp mRNA linear EST 01-MAR-2000
LOCUS
DEFINITION
UI-HF-BROP-a]x-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075813 5', mRNA sequence.
ACCESSION
AM502654
VERSION
AM502654.1 GI:7117309
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 292)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 forward.
FEATURES
source
1..292
Location/Qualifiers

FEATURES
source1..292
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075813"
/clone_11b="NIH_MGC_52"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
51 a 84 c 105 g 52 t
ORIGIN

Query Match 82.0%; Score 16.4; DB 9; Length 292;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 acggtcgagcagctgac 19
|||||
Db 46 ACGGTCGGCGCTGCTATC 63
RESULT 15
AM501791 338 bp mRNA linear EST 01-MAR-2000
LOCUS
DEFINITION
UI-HF-BROP-a]m-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075260 5', mRNA sequence.
ACCESSION
AM501791
VERSION
AM501791.1 GI:7115654
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 338)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 forward.
FEATURES
source
1..338
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075260"
/clone_11b="NIH_MGC_52"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
56 a 98 c 124 g 60 t
ORIGIN
Query Match 82.0%; Score 16.4; DB 9; Length 338;

FEATURES
source

82.0%; Score 16.4; DB 9; Length 338;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 acggtcggcgagctgac 19
 |||||
 Db 46 ACGGTCGGCGCTCTGATC 63

Search completed: August 7, 2002, 21:15:21
 Job time: 22891 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:16 : Search time 146.61 Seconds
(Without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 tacggcgttcgatgacc 20

Scoring table: IDENTITY_NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/pdata/2/1na/5A.COMB.seq:*
2: /cgn2_6/pdata/2/1na/5B.COMB.seq:*
3: /cgn2_6/pdata/2/1na/6A.COMB.seq:*
4: /cgn2_6/pdata/2/1na/6B.COMB.seq:*
5: /cgn2_6/pdata/2/1na/PCTUS.COMB.seq:*
6: /cgn2_6/pdata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	432	2	US-08-313-185-59 Sequence 59, Appl
2	20	100.0	432	3	US-09-082-614A-59 Sequence 59, Appl
3	20	100.0	620	2	US-08-757-653-135 Sequence 135, App
4	20	100.0	620	2	US-08-757-653-136 Sequence 136, App
5	20	100.0	620	2	US-08-757-653-137 Sequence 137, App
6	20	100.0	620	2	US-08-757-653-138 Sequence 138, App
7	20	100.0	620	2	US-08-757-653-139 Sequence 139, App
8	20	100.0	620	2	US-08-757-653-140 Sequence 140, App
9	20	100.0	706	4	US-08-797-812-24 Sequence 24, Appl
10	20	100.0	970	1	US-08-250-030-1 Sequence 1, Appl
11	20	100.0	970	5	PCT-US95-06790-1 Sequence 1, Appl
12	19	95.0	19	4	US-08-750-088A-71 Sequence 71, Appl
13	18.4	92.0	3447	4	US-08-313-185-57 Sequence 57, Appl
14	18.4	92.0	3447	3	US-09-082-614A-57 Sequence 57, Appl
15	15.8	79.0	1472	1	US-08-622-354-2 Sequence 2, Appl
16	15.8	79.0	2310	1	US-08-622-354-1 Sequence 1, Appl
17	15.2	75.0	4403765	4	US-09-103-840A-2 Sequence 2, Appl
18	15	75.0	27	1	US-08-250-030-9 Sequence 9, Appl
19	15	75.0	27	5	PCT-US95-06790-9 Sequence 9, Appl
20	14.2	71.0	1081	4	US-09-372-422A-33 Sequence 33, Appl
21	14.2	71.0	1153	4	US-09-372-448A-5 Sequence 5, Appl
22	14.2	71.0	2262	2	US-08-674-887A-5 Sequence 5, Appl
23	14.2	71.0	2262	3	US-08-951-844-5 Sequence 5, Appl
24	13.8	69.0	117	1	US-08-289-498A-59 Sequence 59, Appl
25	13.8	69.0	117	5	PCT-US95-10813-59 Sequence 59, Appl
26	13.8	69.0	776	4	US-09-372-422A-43 Sequence 43, Appl
27	13.8	69.0	1100	4	US-09-372-422A-47 Sequence 47, Appl

28	13.8	69.0	1176	3	US-08-911-853-34 Sequence 34, Appl
29	13.8	69.0	1176	4	US-09-479-409-34 Sequence 34, Appl
30	13.8	69.0	1176	4	US-09-479-453-34 Sequence 34, Appl
31	13.8	69.0	1375	4	US-09-372-422A-37 Sequence 37, Appl
32	13.8	69.0	1485	4	US-09-372-422A-39 Sequence 39, Appl
33	13.8	69.0	2394	3	US-09-027-064-1 Sequence 1, Appl
34	13.8	69.0	2394	4	US-09-271-815-1 Sequence 1, Appl
35	13.8	69.0	17612	3	US-08-911-853-29 Sequence 29, Appl
36	13.8	69.0	17612	4	US-09-479-409-29 Sequence 29, Appl
37	13.8	69.0	17612	4	US-09-479-453-29 Sequence 29, Appl
38	13.8	69.0	4403765	4	US-09-103-840A-2 Sequence 2, Appl
39	13.6	68.0	585	4	US-09-404-671-3 Sequence 4, Appl
40	13.6	68.0	686	4	US-09-372-422A-45 Sequence 45, Appl
41	13.6	68.0	699	4	US-08-998-416-705 Sequence 705, App
42	13.6	68.0	999	4	US-09-177-234-7 Sequence 7, Appl
43	13.6	68.0	1087	4	US-09-372-422A-29 Sequence 29, Appl
44	13.6	68.0	1209	1	US-08-314-309A-5 Sequence 5, Appl
45	13.6	68.0	1513	1	US-08-314-309A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Tienli, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/C
Sequence 59, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/C
Sequence 135, Application US/08757653
Patent No. 5843669

GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/C
Sequence 136, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/C
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcggttcgatgaacc 20
|||||
Db 325 TACGCGTTTCGATGAACCC 344

RESULT 8
US-08-757-653-140
Sequence 140, Application US/08757653
Patent No. 584369
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-140

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcggttcgatgaacc 20
|||||
Db 325 TACGCGTTTCGATGAACCC 344

RESULT 9
US-08-797-812-24/C
Sequence 24, Application US/08797812
Patent No. 6228575
GENERAL INFORMATION:
APPLICANT: Gingeras, Thomas A.
APPLICANT: Mack, David
APPLICANT: Chee, Mark S.
APPLICANT: Berne, Anthony J.
APPLICANT: Stryer, Anthony J.
APPLICANT: Ghandour, Ghassan
TITLE OF INVENTION: Chip-Based Species Identification and
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,339
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16528X-018550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 332 TACGGCGGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M. 33,977
REGISTRATION NUMBER: 150.105US1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 671 TACGGCGGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 671 TACGGCGGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHRELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657,0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgcttcgatgaacc 19
|||||
Db 1 TACGGCGTTTCGATGACCC 19

RESULT 13
US-08-313-185-57/c
Sequence 57, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 92.0%; Score 18.4; DB 2; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 tacggcgcttcgatgaacc 20
|||||
Db 1454 TACGGCGTTTCGATGACCC 1435

RESULT 14
US-09-082-614A-57/c
Sequence 57, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 92.0%; Score 18.4; DB 3; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 tacggcgcttcgatgaacc 20
|||||

Db 1454 TACGGTGTTCGATGACCC 1435

RESULT 15

US-08-622-354-2/C

; Sequence 2, Application US/08622354

; Patent No. 5827518

GENERAL INFORMATION:

APPLICANT: WEBB, Bruce A.

APPLICANT: CUI, Liwang

TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE

TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER

STREET: 99 Canal Center Plaza, Suite 300

CITY: Alexandria

STATE: VA

COUNTRY: US

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/622,354

FILING DATE: 27-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685

REFERENCE/DOCKET NUMBER: 434-061

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 684-1111

TELEFAX: (703) 684-1124

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1472 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 190..1155

US-08-622-354-2

Query Match 79.0%; Score 15.8; DB 1; Length 1472;

Best Local Similarity 89.5%; Pred. No. 8;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 taagcgcttcgacgaacc 19

||||| ||||| ||||| |||||

Db 1105 TACGGGTTTACATGACCC 1087

Search completed: August 7, 2002, 21:54:21
Job time: 24016 sec

THIS PAGE IS BLANK

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
 Direct Submission
 JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
 College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
 Korea

FEATURES
 source Location/Qualifiers
 1. 306

/organism="Mycobacterium africanum"
 /strain="ATCC25420"
 /db_xref="ATCC:25420"
 /db_xref="taxon:33894"
 <1. >306
 /gene="rpoB"
 <1. >306
 /gene="rpoB"
 /codon_start=3
 /transl_table=11
 /product="RNA polymerase beta"
 /protein_id="A05514.1"
 /db_xref="GI:5902488"
 /translation="RTVGELIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
 VVAATKEPFGTSQISQPMQNNPLSGLTTHKRRLSALPGGLSRERAGLEVRDVHPSH"

CDS

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
 Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
 |||||||
 Db 5 TACGCTCGCGAGCTGATCC 24

RESULT 2

AF057451 306 bp DNA linear BCT 17-SEP-1999
 LOCUS Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
 DEFINITION AF057451
 VERSION AF057451.1 GI:5902489

KEYWORDS
 SOURCE Mycobacterium bovis
 ORGANISM Mycobacterium bovis

REFERENCE 1 (bases 1 to 306)
 Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
 Kim,E.C., Cha,C.Y. and Kook,Y.H.
 Identification of mycobacterial species by comparative sequence
 analysis of the RNA polymerase gene (rpoB)
 J Clin Microbiol. 37 (6), 1714-1720 (1999)

REFERENCE 2 (bases 1 to 306)
 Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
 Kim,E.C., Cha,C.Y. and Kook,Y.H.
 Identification of mycobacterial species by comparative sequence
 analysis of the RNA polymerase gene (rpoB)
 J Clin Microbiol. 37 (6), 1714-1720 (1999)

TITLE Direct Submission
 JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
 College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
 Korea

FEATURES
 source Location/Qualifiers
 1. 306

/organism="Mycobacterium bovis"
 /strain="ATCC19210"
 /db_xref="ATCC:19210"
 /db_xref="taxon:1765"
 <1. >306
 /gene="rpoB"
 <1. >306
 /gene="rpoB"
 /codon_start=3

FEATURES
 source

1. 306

/organism="Mycobacterium bovis"
 /strain="ATCC19210"
 /db_xref="ATCC:19210"
 /db_xref="taxon:1765"
 <1. >306
 /gene="rpoB"
 <1. >306
 /gene="rpoB"
 /codon_start=3

gene

CDS

/codon_start=3

/transl_table=11
 /product="RNA polymerase beta"
 /protein_id="A05515.1"
 /db_xref="GI:5902490"
 /translation="RTVGELIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
 VVAATKEPFGTSQISQPMQNNPLSGLTTHKRRLSALPGGLSRERAGLEVRDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
 Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
 |||||||
 Db 5 TACGCTCGCGAGCTGATCC 24

RESULT 3

AF057452 306 bp DNA linear BCT 17-SEP-1999
 LOCUS Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
 DEFINITION (rpoB) gene, partial cds.
 ACCESSION AF057452
 VERSION AF057452.1 GI:5902491

KEYWORDS
 SOURCE Mycobacterium bovis BCG.
 ORGANISM Mycobacterium bovis BCG

REFERENCE 1 (bases 1 to 306)
 Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
 Kim,E.C., Cha,C.Y. and Kook,Y.H.
 Identification of mycobacterial species by comparative sequence
 analysis of the RNA polymerase gene (rpoB)
 J Clin Microbiol. 37 (6), 1714-1720 (1999)

REFERENCE 2 (bases 1 to 306)
 Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
 Kim,E.C., Cha,C.Y. and Kook,Y.H.
 Identification of mycobacterial species by comparative sequence
 analysis of the RNA polymerase gene (rpoB)
 J Clin Microbiol. 37 (6), 1714-1720 (1999)

TITLE Direct Submission
 JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
 College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
 Korea

FEATURES
 source Location/Qualifiers
 1. 306

/organism="Mycobacterium bovis BCG"
 /strain="French 1173P2"
 /db_xref="taxon:33892"
 <1. >306
 /gene="rpoB"
 <1. >306
 /gene="rpoB"
 /codon_start=3
 /transl_table=11
 /product="RNA polymerase beta"
 /protein_id="A05516.1"
 /db_xref="GI:5902492"
 /translation="RTVGELIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
 VVAATKEPFGTSQISQPMQNNPLSGLTTHKRRLSALPGGLSRERAGLEVRDVHPSH"

BASE COUNT

56 a 95 c 108 g 47 t

ORIGIN

1. 306

/organism="Mycobacterium bovis BCG"
 /strain="French 1173P2"
 /db_xref="taxon:33892"
 <1. >306
 /gene="rpoB"
 <1. >306
 /gene="rpoB"
 /codon_start=3
 /transl_table=11
 /product="RNA polymerase beta"
 /protein_id="A05516.1"
 /db_xref="GI:5902492"
 /translation="RTVGELIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
 VVAATKEPFGTSQISQPMQNNPLSGLTTHKRRLSALPGGLSRERAGLEVRDVHPSH"

gene

CDS

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"
 /protein_id="A05516.1"
 /db_xref="GI:5902492"
 /translation="RTVGELIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
 VVAATKEPFGTSQISQPMQNNPLSGLTTHKRRLSALPGGLSRERAGLEVRDVHPSH"

Query Match 100.0%; Score 20; DB 1; Length 306;
 Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
 |||||||

Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 4

AF057453 306 bp DNA linear BCT 17-SEP-1999

LOCUS AF057453

DEFINITION Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057453

VERSION AF057453.1 GI:5902493

KEYWORDS

SOURCE Mycobacterium bovis BCG.

ORGANISM Mycobacterium bovis BCG.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y., and Kook,Y.H.

TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)

AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J., and Cha,C.Y.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Yongsong-dong, Chongno-gu, Seoul 110-799, Korea

FEATURES

source 1..306

location/Qualifiers

/organism="Mycobacterium bovis BCG"

/strain="Tokyo T172"

/db_xref="taxon:33892"

<1..>306

/gene="rpoB"

<1..>306

/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="AAD5517.1"

/db_xref="GI:5902494"

/translation="RTVGEILNQIRVGSRMERYRERMTQDVEAITPOTLINIRP VVAATKEFGTQSLSQFMQNNPISGLTHKRRLSALPGCLSRERAGLEVVDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgcgagctgattcc 20

|||||

Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 5

AF057454 306 bp DNA linear BCT 08-OCT-1999

LOCUS AF057454

DEFINITION Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057454

VERSION AF057454.1 GI:5902495

KEYWORDS

SOURCE Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene

JOURNAL Patent: US 6242584-A 2 05-JUN-2001;

FEATURES

source 1..306

/organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgcgagctgattcc 20

|||||

REFERENCE 1 (bases 1 to 306)

AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y., and Kook,Y.H.

TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)

AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J., and Cha,C.Y.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Yongsong-dong, Chongno-gu, Seoul 110-799, Korea

FEATURES

source 1..306

location/Qualifiers

/organism="Mycobacterium tuberculosis"

/strain="H37Rv; ATCC27294"

/db_xref="ATCC:27294"

/db_xref="taxon:1773"

<1..>306

/gene="rpoB"

<1..>306

/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="AAD5518.1"

/db_xref="GI:5902496"

/translation="RTVGEILNQIRVGSRMERYRERMTQDVEAITPOTLINIRP VVAATKEFGTQSLSQFMQNNPISGLTHKRRLSALPGCLSRERAGLEVVDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgcgagctgattcc 20

|||||

Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 6

ARI57003 306 bp DNA linear PAT 08-AUG-2001

LOCUS ARI57003

DEFINITION Sequence 2 from patent US 6242584.

ACCESSION ARI57003

VERSION ARI57003.1 GI:15125707

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene

JOURNAL Patent: US 6242584-A 2 05-JUN-2001;

FEATURES

source 1..306

/organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgcgagctgattcc 20

|||||

```

Db      5  TACGGTCGGCAGCTGATCC 24

RESULT  7
LOCUS   AR157007 306 bp  DNA  linear  PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION AR157007
VERSION   AR157007.1 GI:15125711
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS   Kook,Y.-H. and Kim,B.-J.
TITLE     Method for identifying mycobacterial species by comparative
          sequence analysis of ipob gene
JOURNAL   Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
  source   1..306
            /organism="unknown"
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  tacggtcggcagctgattcc 20
    |||||||||||||||||||
Db 5  TACGGTCGGCAGCTGATCC 24

RESULT  8
LOCUS   AR157008 306 bp  DNA  linear  PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION AR157008
VERSION   AR157008.1 GI:15125712
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS   Kook,Y. and Kim,B.
TITLE     Method for identifying mycobacterial species by comparative
          sequence analysis of ipob gene
JOURNAL   Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
  source   1..306
            /organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  tacggtcggcagctgattcc 20
    |||||||||||||||||||
Db 5  TACGGTCGGCAGCTGATCC 24

RESULT  9
LOCUS   AR157042 306 bp  DNA  linear  PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION AR157042
VERSION   AR157042.1 GI:15125746
KEYWORDS
SOURCE   Unknown.

```

```

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS   Kook,Y. and Kim,B.
TITLE     Method for identifying mycobacterial species by comparative
          sequence analysis of ipob gene
JOURNAL   Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
  source   1..306
            /organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  tacggtcggcagctgattcc 20
    |||||||||||||||||||
Db 5  TACGGTCGGCAGCTGATCC 24

RESULT  10
LOCUS   AR157051 306 bp  DNA  linear  PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION AR157051
VERSION   AR157051.1 GI:15125755
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS   Kook,Y. and Kim,B.
TITLE     Method for identifying mycobacterial species by comparative
          sequence analysis of ipob gene
JOURNAL   Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
  source   1..306
            /organism="unknown"
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1  tacggtcggcagctgattcc 20
    |||||||||||||||||||
Db 5  TACGGTCGGCAGCTGATCC 24

RESULT  11
LOCUS   MSGRIFRNAP 432 bp  DNA  linear  BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
          resistance gene, complete cds.
ACCESSION L05910.1 GI:149991
VERSION   L05910.1
KEYWORDS  RNA polymerase beta-subunit; rifampicin resistance.
SOURCE    Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM  Mycobacterium tuberculosis
          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
          Actinomycetales; Corynebacteriineae; Mycobacteriaceae;
          Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
          Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
          Detection of rifampicin-resistance mutation in Mycobacterium
          tuberculosis
          JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

```

FEATURES

Location/Qualifiers

1..432

/organism="Mycobacterium tuberculosis"

/strain="H37"

/db_xref="taxon:1773"

<1..>432

/codon_start=1

/transl_table=11

/product="RNA polymerase beta subunit"

/protein_id="AAB59068.1"

/db_xref="GI:148992"

/translation="GNRLRTVGLIQNIRVGSRMERYRERMTTQDVEATPQTL
INIRPVAAIKKEFGTSOLFMDQNNPLSGLTKRRRLSALGPGGLSRRERAGIEVRDV
HPSHYCRMCPTEPECPNIGLISLVARVNEFCFETPYR"

variation

/phenotype="rifampicin resistant in association with
mutation 234 G"

variation

/phenotype="rifampicin resistant"

188

/replace="c"

variation

/phenotype="rifampicin resistant"

191

/replace="c"

variation

/phenotype="rifampicin resistant in association with
mutation 203 T"

194

/replace="c"

variation

/phenotype="rifampicin resistant"

203

/replace="t"

variation

/phenotype="rifampicin resistant"

/replace="t"

208..210

/phenotype="rifampicin resistant"

/replace="a"

232

/phenotype="rifampicin resistant"

/replace="g"

232

/phenotype="rifampicin resistant"

/replace="a"

233

/phenotype="rifampicin resistant"

/replace="g"

233

/phenotype="rifampicin resistant"

/replace="c"

234

/phenotype="rifampicin resistant"

/replace="g"

247..248

/phenotype="rifampicin resistant"

/replace="ca"

248

/phenotype="rifampicin resistant"

/replace="g"

248

/phenotype="rifampicin resistant"

/replace="t"

254

/phenotype="rifampicin resistant"

/replace="c"

BASE COUNT

77 a 140 c 148 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgattcc 20
|||||
Db 18 TACGTCGCGAGCTGATCC 37

RESULT 12

AR067448

LOCUS

DEFINITION

AR067448

ACCESSION

AR067448

VERSION

AR067448.1 GI:5998670

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 432)

AUTHORS

Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
Bodmer, T.

TITLE

Rapid detection of antibiotic resistance in mycobacterium
tuberculosis

JOURNAL

Patent: US 5851763-A 59 22-DEC-1998;

FEATURES

Location/Qualifiers

1..432

/organism="unknown"

BASE COUNT

77 a 139 c 149 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgattcc 20
|||||
Db 18 TACGTCGCGAGCTGATCC 37

RESULT 13

I50706

LOCUS

DEFINITION

Sequence 1 from patent US 5643723.

ACCESSION

I50706

VERSION

I50706.1 GI:2472409

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 970)

AUTHORS

Persing, D.H., Hunt, J.J., Young, K.K.Y., Peimlee, T.A., Roberts, G.D.
and Whelan, A.Christian.

TITLE

Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens

JOURNAL

Patent: US 5643723-A 1 01-JUL-1997;

FEATURES

Location/Qualifiers

1..970

/organism="unknown"

BASE COUNT

182 a 302 c 330 g 156 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgattcc 20
|||||
Db 261 TACGTCGCGAGCTGATCC 280

RESULT 14

AX111339

LOCUS

DEFINITION

Sequence 2072 from Patent WO0123604.

ACCESSION

AX111339

VERSION

AX111339.1 GI:13927631

KEYWORDS

SOURCE

Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
REFERENCE
AUTHORS Bergeron,M.G., Bolissnot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
source
Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 taacgtcgagcagctgattcc 20
|||||
Db 1137 TACGTCGCGAGCTGATCC 1156
RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION
gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3853)
REFERENCE
AUTHORS Imboden,P., Toller,R., Marchesi,F., Telenti,A., Bodmer,T.,
Cole,S., Schopfer,K. and Burkart,T.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3853)
AUTHORS Imboden,P.
TITLE Direct Submision
JOURNAL Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehstrasse 51, Berne,
3010, Switzerland
FEATURES
source
Location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
/gene="rpoB"
/codon_start=1
/transl_table=11
/product="RNA-polymerase beta subunit"
/protein_id="AA02042.2"
/db_xref="GI:7144499"
/translation="MLEGCIADSRQSKTAASPSRPOSSNNNSVPGANRYSPAKL
REPLEVYGLDVQTDSEFWLIGSPRMRESAERGVNPGLEEVLYELSPIDFSG
MSLSFSDPREDDKAVDECKDKDMYAAPLFTAPFINNNGEIKSOTYFMGDFPM
TEKGFTIINGTERVVSOLYRSRGVDEETIDKSTDKLHSAVKVIPSRGAMLEFDYDK
RDYGVIRIDRKROPVTVILKALGWTSEQIVERFGSEIKRSTLEKDNVTGDEALLD
IKLRGPEPTKESAQTILENLFKEKRYDLARVGRYKVNKKLGLHVGEPITTSFLT

EEDVATIEYLVRLHSGOTTMTVPGVEVEFETDDIDHFGNRRRLTVGELLIONQIRVG
MSMERVYREMTQDVEAITPQTLIRPVVAAIKFEFTSQSOPMDONNPLSGLT
HKRRSLALGGSLSRERAGLEVDPVHSHVGMCPITTEPGNIGLIGSLSVARVP
EGFIEIPYRKVGVGVSVDGIVYLTADEDESHVVAQANSPIDADGRFEPVRLRRAG
EVEYVSSSEYDYNDVSPROMVSATAMIPFLEHDDANRALMGANMOQAVPLVNSEAP
LVGTGMELRALIDAATSSSOESGVIEVSADYITVMNDGTRRTYRMRKPARSNHGT
ANOCPIVDAGDRVAGOVVADGCTDGENALGNLVAIMPENHVEDAIILSNL
VEEDVLTSIHIEHEIDARDTKLGAETIPNDIPNISDEVLADDERGIVRIGAEVRDG
DILVGVTPKGETELPPEERLLRAIFGEKAREVDTSKVPHGSGKVGIRVFSRED
EDELPAVGNELVAVVAAQKRKISDGKLAGRHGKNGVIGKILPEEDMPLADGTPVDI
ILNTHGVPRRMNIGQILETHLGMCAHSGKVDKAKVDPDMAARLPDELLERONRAIYS
TPVFDGQENELGGLSCTLPNRDGDVLVADGKAMLPDGRSGEPFPYPTVGVMTYM
KLHLVLVDKLIHARSTGYSMTIQOPLGKRAQFGQRFGEKMECMAQVGAAYTLQELL
TKS"
BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 taacgtcgagcagctgattcc 20
|||||
Db 1712 TACGTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 21:51:38
Job time: 23873 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:17 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 taacgcgttcgtatgacc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estha:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	396	10	BF220419 NXCI_146-
2	17.4	87.0	399	10	BF169611 NXCI_125-
3	17.4	87.0	452	10	BG040291 NXCI_110-
4	17.4	87.0	539	9	AA556698 553 lobi
5	17.4	87.0	545	10	BF777209 NXCI_066
6	17.4	85.0	234	10	W06754 SMEST0390 S
7	17.4	85.0	579	10	T24127 SMEST0325 S
8	16.8	84.0	277	9	AA734164 VS1912.r
9	16.4	82.0	576	10	BF252921 EST420184
10	16.4	82.0	624	10	BE896357 601439015
11	16.4	82.0	631	12	BH615799 BMAC304F
12	16.4	82.0	961	12	AG141490 Pan trogl
13	15.8	79.0	213	9	AM064407 SP0996 KR
14	15.8	79.0	436	9	A1496312 SB0508.Y
15	15.8	79.0	582	12	AL147937 Anopheles
16	15.8	79.0	637	10	BG908684 Tair1170D
17	15.8	79.0	650	10	BG908616 Tair1169H

c 18	15.8	79.0	752	12	CNS03678	AL229661 Tetradon
c 19	15.8	79.0	775	12	A2125549	A2125549 OSJNB009
c 20	15.8	79.0	885	12	CNS0280Q	AL189251 Tetradon
c 21	15.8	79.0	913	10	BF204833	BF204833 601867133
c 22	15.8	79.0	1029	12	CNS0549K	AL320465 Tetradon
c 23	15.8	79.0	1411	10	B1663170	B1663170 603286791
c 24	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
c 25	15.4	77.0	248	10	BG140300	BG140300 EST480742
c 26	15.4	77.0	269	9	AV640876	AV640876 AV640876
c 27	15.4	77.0	384	10	BM077908	BM077908 PD21906.Y
c 28	15.4	77.0	390	9	AV644609	AV644609 AV644609
c 29	15.4	77.0	467	12	CNS03FUV	AL242176 Tetradon
c 30	15.4	77.0	474	9	AV396989	AV396989 AV396989
c 31	15.4	77.0	489	9	AM618736	AM618736 EST320722
c 32	15.4	77.0	497	9	AV643117	AV643117 AV643117
c 33	15.4	77.0	508	9	AV642711	AV642711 AV642711
c 34	15.4	77.0	518	9	AV642141	AV642141 AV642141
c 35	15.4	77.0	531	9	AV642766	AV642766 AV642766
c 36	15.4	77.0	532	10	B1506216	B1506216 B1170018A
c 37	15.4	77.0	536	12	A0783856	A0783856 HS_2001_A
c 38	15.4	77.0	548	12	A0497017	A0497017 HS_5197_B
c 39	15.4	77.0	566	9	AV631818	AV631818 AV631818
c 40	15.4	77.0	788	10	BE566696	BE566696 601339653
c 41	15.2	76.0	146	10	BM096759	BM096759 Ebma07_SQ
c 42	15.2	76.0	200	10	BM098906	BM098906 EBP105_SQ
c 43	15.2	76.0	205	12	A2577000	A2577000 06405_Sho
c 44	15.2	76.0	269	10	BF953380	BF953380 RC3-NN019
c 45	15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
BF220419 396 bp mRNA linear EST 08-NOV-2000
LOCUS NXCI_146 A06.F NXCI (NsF Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NXCI_146 A06 5', mRNA sequence.

ACCESSION BF220419.1 GI:11126551

VERSION BF220419.1

KEYWORDS EST.

SOURCE lobiolly pine.

ORGANISM Pinus taeda

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

TITLE Sederoff, R.

JOURNAL Molecular Basis of Wood Formation in the Pine Megagenome

COMMENT Unpublished (2000)

Contact: Johnson, Arthur

North Carolina State University

Tel: 919 515 7800

Fax: 919 515 7801

Email: ajohnson@unity.ncsu.edu

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..396

/organism="Pinus taeda"

/strain="Coastal plain lobiolly pine from North Carolina"

/db_xref="taxon:3352"

/clone="NXCI_146 A06"

/clone_lib="NXCI (NsF Xylem Compression wood Inclined)"

/tissue_type="xylem"

/cell_type="Compression"

/dev_stage="juvenile"

/lab_host="Xyl-Blue"

/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: Xho I

: The library is from early (spring) wood, taken from

three six-year old trees (three different genotypes), in

the juvenile phase. These trees were induced to form

compression wood by bending to a 45 degree angle and tying

them to the ground. Differentiating xylem was harvested

from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dt primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTGGCAGCAG'.

BASE COUNT 71 a 84 c 122 g 110 t 9 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgttcgatgaacc 20
||||| |||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 2
BFI69611 399 bp mRNA linear EST 30-OCT-2000
LOCUS NCBI_125_C05_F NCBI (Nsf Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NCBI_125_C05_5', mRNA sequence.
ACCESSION BFI69611 GI:11054228
VERSION BFI69611.1 GI:11054228
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 399)
Sederoff, R.

AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome
TITLE Unpublished (2000)
JOURNAL Contact: Johnson, Arthur
COMMENT North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers
1..399

/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NCBI_125_C05"
/clone_1kb="NCBI (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of
all three genotypes was used for the library. Oligo-dt
primed cDNA was directionally cloned into the EcoRI-XhoI
Bluescript SK vector arms. NOTE: The sequences contain a
'cDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTGGCAGCAG'."

BASE COUNT 71 a 84 c 121 g 121 t 2 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgttcgatgaacc 20
||||| |||||||||

Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 3
BG040291 452 bp mRNA linear EST 24-JAN-2001
LOCUS NCBI_110_F06_F NCBI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
DEFINITION clone NCBI_110_F06_5', mRNA sequence.
ACCESSION BG040291 GI:12482876
VERSION BG040291.1 GI:12482876
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 452)
Sederoff, R.

AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome
TITLE Unpublished (2000)
JOURNAL Contact: Johnson, Arthur
COMMENT North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers
1..452

/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NCBI_110_F06"
/clone_1kb="NCBI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dt primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTGGCAGCAG'."

BASE COUNT 71 a 122 c 146 g 95 t 18 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgttcgatgaacc 20
||||| |||||||||
Db 329 ACGGCGCTTCGATGAACCC 347

RESULT 4
AA556698 539 bp mRNA linear EST 28-AUG-1998
LOCUS AA556698 533 loblolly pine CA Pinus taeda cDNA clone ICAB4c, mRNA sequence.
ACCESSION AA556698
VERSION AA556698.1 GI:3365713
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE 1 (bases 1 to 539)

BASE COUNT 71 a 122 c 146 g 95 t 18 others

AUTHORS Allona, I., Quinn, M., Shoop, E., Swope, K., St. Cyr, S., Carlis, J., Riedl, J., Retzel, E., Campbell, M.M., Sedoreff, R. and Whetten, R.W.
 TITLE Analysis of xylem formation in pine by cDNA sequencing
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
 MEDLINE 98356220
 COMMENT Contact: Ross Whetten
 Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhetten@uncy.ncsu.edu

FEATURES

Seq primer: T3.

Location/Qualifiers

1..539
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="1CAB4G"
 /clone_lib="loblolly pine CA"
 /tissue_type="Xylem"
 /lab_host="SOLR"
 /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
 The result of subtraction of C library with N library.
 Immature xylem from the underside of inclined stems of
 differentiating compression wood was subtracted with
 Immature xylem from the side of inclined stems of
 differentiating wood. A mixture of four genotypes were
 used. Oligo-dr primed cDNA was directionally cloned into
 the EcoRI-XhoI lambda-ZAP vector arms"
 BASE COUNT 102 a 120 c 156 g 150 t 11 others
 ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 539;
 Best Local Similarity 94.7%; Pred. No. 78;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 accgagcttcgattgaacc 20
 ||||| ||||| ||||| |||||
 Db 145 accgagcttcgattgaacc 163

RESULT 5 545 bp mRNA linear EST 12-JAN-2001
 LOCUS BF777209
 DEFINITION NXSI_066_E05_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
 clone NXSI_066_E05 5', mRNA sequence.
 ACCESSION BF777209
 VERSION BF777209.1 GI:12125109
 KEYWORDS EST.
 SOURCE loblolly pine.
 ORGANISM Pinus taeda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 Sederoff, R.
 1 (bases 1 to 545)
 Molecular Basis of Wood Formation in the Pine Megagenome
 Unpublished (2000)
 Contact: Johnson, Arthur
 North Carolina State University
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: ajohnson@uncy.ncsu.edu
 Seq primer: T3.

FEATURES

Location/Qualifiers

1..545
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXSI_066_E05"
 /clone_lib="NXSI (Nsf Xylem Side wood Inclined)"

/tissue_type="Xylem"
 /cell_type="Side"
 /dev_stage="juvenile"
 /lab_host="XLI-Blue"
 /note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
 ; The library is from early (spring) wood, taken from
 three six-year old trees (three different genotypes), in
 the juvenile phase. These trees were induced to form side
 wood by bending to a 45 degree angle and tying them to the
 ground. Differentiating xylem was harvested from the sides
 of the inclined stems, and a mixture of all three
 genotypes was used for the library. oligo-dr primed cDNA
 was directionally cloned into the EcoRI-XhoI Bluescript SK
 vector arms. NOTE: The sequences contain a 'cDNA adapter'
 between the EcoRI site and the start of the EST. The
 adapter sequence is 'AATTCGGCAGCAG'."
 BASE COUNT 92 a 142 c 167 g 132 t 12 others
 ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 545;
 Best Local Similarity 94.7%; Pred. No. 78;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 accgagcttcgattgaacc 20
 ||||| ||||| ||||| |||||
 Db 256 accgagcttcgattgaacc 274

RESULT 6 234 bp mRNA linear EST 01-JUL-1996
 LOCUS W06754/c
 DEFINITION SMeST0390 Schistosoma mansoni, adult worm, Gloria Franco
 Schistosoma mansoni cDNA clone SMPB73 3' end, mRNA sequence.
 ACCESSION W06754
 VERSION W06754.1 GI:1444974
 KEYWORDS EST.
 SOURCE Schistosoma mansoni.
 ORGANISM Schistosoma mansoni.
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 1 (bases 1 to 234)
 Franco, G.R. and Pena, S.D.J.
 Franco, G.R. and Pena, S.D.J., Unpublished
 Unpublished (1996)
 Contact: Franco G.R. and Pena S.D.J.
 Laboratorio de Genetica-Bioquímica, Departamento de Bioquímica
 Imunologia
 Instituto de Ciencias Biológicas, Universidade Federal de Minas
 Gerais
 Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
 Tel: (5531)4415611
 Fax: (5531)4415409
 Email: gfranco@mono.icb.ufmg.br
 Seq primer: M13 Forward.

FEATURES

Location/Qualifiers

1..234
 /organism="Schistosoma mansoni"
 /strain="NMRI"
 /db_xref="taxon:6183"
 /clone="SMPB73"
 /clone_lib="Schistosoma mansoni, adult worm, Gloria
 Franco"
 /lab_host="DH10B, JM109"
 /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
 Total cellular RNA from male and female adult worms was
 extracted according to a modification (Puisant, C. and
 Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
 Guanidine thiocyanate procedure (Chomczynski, P. and
 Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
 RNA was purified by Oligo dt column and cDNA was
 synthesized as described previously (Adams, M. D. et al.
 Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (Jafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaa 17
|||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 7
T24127/c 579 bp mRNA linear EST 27-FEB-1995
LOCUS SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA SMPBC65 3', mRNA sequence.
T24127
T24127.1 GI:529730
EST.
Schistosoma mansoni.
Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoidae; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 579)
Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.
and Pena, S.D.J.
Identification of new Schistosoma mansoni genes by the EST strategy
using a directional cDNA library
Gene 152, 141-147 (1995)
95137379
Contact: Franco G.R. and Pena S.D.J.
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica
Imunologia
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seg primer: M13 Forward.
Location/Qualifiers
1..579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone.lib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector. Site.1: NotI; Site.2: HindIII;
total cellular RNA from male and female adult worms was
extracted according to a modification (Pissant, C. and
Houdeline, L. M. Biofeedback 8, 148-149, 1990) of the
Guandine thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dt column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
two fold molar excess of a NotI/HindIII digested plasmid
DNA (Jafmid BA vector, a phagemid derived from pEMBL,
Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and
electroporated into E. coli strain DH10B (BRL). The

library was amplified and further selected for clones
containing long inserts (>500 bp) by purification of the
plasmid DNA from a fragment of a 1% low-melting-point
agarose gel, containing the smear of the library and
electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaa 17
|||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 8
AA734164 277 bp mRNA linear EST 07-JAN-1998
LOCUS vsl9g12.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA
DEFINITION (MOUSE);, mRNA sequence.
AA734164
AA734164.1 GI:2755831
EST.
house mouse.
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 277)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMNI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:619998
Trace considered overall poor quality
Seg primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..277
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138726"
/clone.lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker. Site.1: EcoRI; Site.2: NotI; Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
(5'-TGTTCGATCTGAGTGGACGGCCCGCTTTTCTTTTCTTTTCTTTT
T 3') ; double-stranded cDNA was ligated to Eco RI
adaptors (AATTCGATCTCTG), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p7T73
vector. Library constructed by Bob Barstead."

BASE COUNT 64 a 59 c 92 g 62 t

Query Match 84.0%: Score 16.8; DB 9: Length 277;
Best Local Similarity 90.0%: Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cagcgcttcgatgaaccc 20
||||| ||||||| |||||
Db 47 TACGGCATTTCGATGACACC 66

RESULT 9
BF252921 576 bp mRNA linear EST 15-NOV-2001
LOCUS BF252921/c
DEFINITION Imitis spherule cDNA library Coccidioides
ACCESSION BF252921
VERSION BF252921.1 GI:16933064
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
REFERENCE Eukaryote: Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oxygenales; mitosporic Oxygenales; Coccidioides.
AUTHORS Gardner, M.J. and Kirkland, T.
TITLE 1 (bases 1 to 576)
JOURNAL Generation of ESTs from Coccidioides immitis spherule cDNA library
COMMENT Unpublished (2000)
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Location/Qualifiers
1..576
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIABC49"
/clone_1lb="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 113 a 186 c 176 g 101 t
ORIGIN

Query Match 82.0%: Score 16.4; DB 10: Length 576;
Best Local Similarity 94.4%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cggcgcttcgatgaaccc 20
||||| ||||||| |||||
Db 241 CGCGCTTCGATGACACC 224

RESULT 10
BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS BE896357
DEFINITION 601439015F1 NIH_MGC_72 Homo sapiens cDNA IMAGE:3924266 5',
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs.femail.nih.gov
Tissue Procurement: ATCC/DC/DPF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_1lb="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 155 a 209 c 150 g 110 t
ORIGIN

Query Match 82.0%: Score 16.4; DB 10: Length 624;
Best Local Similarity 94.4%: Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cggcgcttcgatgaaccc 20
||||| ||||||| |||||
Db 580 CGCGCTTCGATGACACC 597

RESULT 11
BH615799 631 bp DNA linear GSS 28-JAN-2002
LOCUS BH615799
DEFINITION BMBAC304F01SP6_P5U Brugia malayi genomic Bac library 3 Brugia
ACCESSION BH615799
VERSION BH615799.1 GI:18380487
KEYWORDS GSS.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryote: Metazoa; Nematoda; Chromadorea; Spturida; Filarioidea;
Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 631)
AUTHORS Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
J., Guiliiano, D., Slatko, B., and Blaxter, M.
TITLE Genome survey sequences from the human parasitic nematode Brugia
malayi
JOURNAL Unpublished (2000)
COMMENT Contact: Blaxter, M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JF, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by the
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAEB, University of Edinburgh,
Edinburgh, UK.
Seq primer: SP6 (ATTAGTCACTATAG)
Class: BAC ends.
Location/Qualifiers
1..631
/organism="Brugia malayi"

/strain="TRS"
/db_xref="taxon:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBAC3.6; Site_1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Baxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

BASE COUNT 196 a 94 c 142 g 199 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 631;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 accgagtttcgataacc 19
|||||

Db 606 ACGGCGTTGATGATGCC 623

RESULT 12
AG141490 961 bp DNA linear GSS 08-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
DEFINITION
ACCESSION AG141490
VERSION AG141490.1 GI:16671168
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-001J13.TJ.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library RPCI-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 961)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : ECORI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 961
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J13.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 255 a 299 c 145 g 252 t 10 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 961;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 accgagtttcgataacc 19
|||||

Db 746 ACGGCGTTGATGATGCC 729

RESULT 13
AM064407/c 213 bp mRNA linear EST 07-DEC-2000
LOCUS SP05936 KRIIB Human CD4 intrathymic T-cell cDNA library Homo sapiens
DEFINITION
ACCESSION AM064407
VERSION AM064407.1 GI:8888344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-G., Yoo, H.-S., Lee, I.-C., Park, J.-H., Kim, Y.-S. and Lee, C.-C.
TITLE Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis
JOURNAL Genomics 70 (1), 1-18 (2000)
MEDLINE 20541704
COMMENT Contact: Sung-Ho Goh
Genome Center
Korea Research Institute of Bioscience and Biotechnology
Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea
Tel: 82-42-860-4473
Fax: 82-42-860-4479
Email: gohsh@mail.kribd.re.kr
Seq primer: T7
High quality sequence stop: 213
POLYA-No.

FEATURES
source
1. 213
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KRIIB Human CD4 intrathymic T-cell cDNA library"
/tissue_type="Thymus"
/dev_stage="CD3+4+8- single positive stage"
/note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3+4+8-T-cell, adaptor ligated, amplified with PCR, and cloned into pGEM-T vector."

BASE COUNT 41 a 59 c 72 g 40 t 1 others
ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 213;
Best Local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgagtttcgataacc 20
|||||

Db 43 ACGGCGTTGATGATGCC 25

RESULT 14
A1496312 436 bp mRNA linear EST 30-NOV-2001
LOCUS sp0508.y1 Gm-cl1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl1004-7888 5' similar to TR:Q92388 Q92388 CRG1 GENE. ;, mRNA
DEFINITION
ACCESSION A1496312

VERSION A1496312.1 GI:4397315
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 436)
 AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Hunttsville, AL 35801 For further information call: (800)-533-4363 or contact via email: cduresgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 386
 POLYA-No.

FEATURES
 source Location/Qualifiers
 1..436
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-7888"
 /clone_11b="Gm-cl004"
 /tissue_type="root"
 /lab_host="XL10-Gold"
 /note="Vector: pBluescript II Xr; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGGAGAGAGAGAGAGACTGCTCGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters, and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II Xr Predigested vector (pBluescript II SK(+)) that had been digested with EcoRI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. Blue colonies 9n-15) have been sequenced, and possess putative cDNA inserts. This library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, email: paul.keim@nau.edu, virginia.coryell@nau.edu"

BASE COUNT 90 a 174 c 96 g 76 t
 ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 436;
 Best Local Similarity 89.5%; Pred. No. 5.3e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 acggcgcttcgatgaacc 20
 Db 185 ACCGCGCTTCGATGAACCC 203

RESULT 15
 LOCUS CNS01K68/C
 DEFINITION Anopheles gambiae GSS sp6 end of clone 16E18 of NotreDame1 library from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
 ACCESSION AL147937
 VERSION AL147937.1 GI:7006083
 KEYWORDS GSS.
 SOURCE African malaria mosquito.
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 582)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

REFERENCE 2 (bases 1 to 582)
 AUTHORS Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.
 TITLE Direct Submission
 JOURNAL Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France

COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES
 source Location/Qualifiers
 1..582
 /organism="Anopheles gambiae"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone="16E18"
 /clone_11b="Notredame1"
 /note="end : sp6"

BASE COUNT 160 a 124 c 136 g 153 t 9 others
 ORIGIN

Query Match 79.0%; Score 15.8; DB 12; Length 582;
 Best Local Similarity 89.5%; Pred. No. 5.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 acggcgcttcgatgaacc 20
 Db 320 ACCGCGCTTCGATGAACCC 302

Search completed: August 7, 2002, 21:15:20
 Job time: 22890 sec

PS Claim 4; Page 4; 43pp; English.

XX The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp

CC 2611-2592). It is used with the forward primer given in AAA49823

CC and with the sequencing primers given in AAA49825 and AAA49826 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-62) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), gyrA

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

S0 Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

Db 1 tacggcggttcgatgaacc 20

|||||

RESULT 2

AAA49826

ID AAA49826 standard; DNA; 20 BP.

XX

AC AAA49826;

XX

DT 25-SEP-2000 (first entry)

XX

DE *Mycobacterium tuberculosis* rpoB gene sequencing primer rpoB-3s.

XX

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

KM ss.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO200036142-A1.

XX

PD 22-JUN-2000.

XX

PF 10-DEC-1999; 99WO-CA01177.

XX

PR 11-DEC-1998; 98US-0111794.

XX

PA (VIST-) VISIBLE GENETICS INC.

XX

PI Shipman R;

XX

PI WPI; 2000-431611/37.

DR

XX

PT Method for the detection and characterization of *Mycobacterium*

PT tuberculosis with antibiotic resistance in a sample -

XX

PS Claim 4; Page 5; 43pp; English.

XX

CC The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp

CC 2611-2592). It is used with the forward primer given in AAA49825 and

CC with the amplification primers given in AAA49823 and AAA49824 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-62) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rfs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

S0 Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

Db 1 tacggcggttcgatgaacc 20

|||||

RESULT 3

AAQ61457/G

ID AAQ61457 standard; DNA; 432 BP.

XX

AC AAQ61457;

XX

DT 17-MAY-1994 (first entry)

XX

DE *M. tuberculosis* rpoB gene fragment.

XX

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;

KM mutant; ss.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO9322454-A.

XX

PD 11-NOV-1993.

XX

PF 30-APR-1993; 93WO-EP01063.

XX

PR 17-SEP-1992; 92FR-0011098.

XX

PR 30-APR-1992; 92US-0875940.

XX

PR 14-AUG-1992; 92US-0929206.

XX

PR 16-APR-1993; 93FR-0004545.

XX

PA (ASST-) ASSISTANCE PUBLIQUE.

PA (INSP) INST PASTEUR.

PA (MEDI-) MEDICAL RES COUNCIL.

PA (UYBE-) UNIV BERNE.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

PI Young D, Zhang Y;

XX

DR WPI; 1993-368812/46.

DR P-PSDB; AAR51372.

XX

PT Rapid detection of antibiotic resistance in *Mycobacterium* - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in *katG*, *rpoB* or *rpsL* genes
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain *rpoB* genes from rifampicin-
CC resistant *Mycobacterium lepreae* strains. A comparison with the
CC sequence of the *rpoB* gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from *M. tuberculosis* (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA: 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE *Mycobacterium tuberculosis rpoB* gene (rifampin resistance).
XX
KM Antibiotic resistance; *rpoB* gene; rifampin resistance; ss.
XX
OS *Mycobacterium tuberculosis*.
XX
FH Key Location/Qualifiers
FT primer_bind /*cag- a complement(41..60)
FT /*cag- a primer of AAA49823*
FT primer_bind 372..391
FT /*cag- b
FT /*note- "primer of AAA49824"
XX
XX MO200036142-A1.
XX
XX 22-JUN-2000.
XX
XX 10-DEC-1999; 99WO-CA01177.
XX
XX 11-DEC-1998; 98US-0111794.
XX
XX (VIST-) VISIBLE GENETICS INC.
XX
XX Shipman R;
XX
XX WPI; 2000-431611/37.
XX
XX Method for the detection and characterization of *Mycobacterium*
XX tuberculosis with antibiotic resistance in a sample -
XX
XX Disclosure; Page 5; 43pp; English.
XX
XX The present sequence is that of the *Mycobacterium tuberculosis*
XX *rpoB* (rifampin resistance) gene (bp2161-2640). Amplification and
XX cycle sequencing primers (see AAA49823-62) are used for the detection
XX and analysis of antibiotic resistance-associated mutations in
XX defined regions of *rpoB* (rifampin), *katG* (isoniazid), *oxyR-aphc* PR
XX (isoniazid), *mabA* (isoniazid), *rpsL/s12* (streptomycin), 16S/r16S

CC (streptomycin), *embB* (ethambutol), *pncA* (pyrazinamide), *gyrA*
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpoB*, *katG*, *rpsL/s12*
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA: 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE *rpoB* gene fragment (mutant) from *Mycobacterium tuberculosis*.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; *Thermus*;
XX
KM *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
XX
KM *Staphylococcus*; Identification; detection; ds.
XX
OS *Mycobacterium tuberculosis*.
XX
XX WO9615267-A1.
XX
XX 23-MAY-1996.
XX
XX 09-NOV-1995; 95WO-US14673.
XX
XX 30-AUG-1995; 95US-0520946.
XX
XX 09-NOV-1994; 94US-0337164.
XX
XX 09-MAR-1995; 95US-0402601.
XX
XX 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Brow MAD, Dahlberg JE, Fors L, Helsler LM, Lyamichev VI;
XX Oldenburg MC, Olive DM;
XX
XX WPI; 1996-259862/26.
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection
XX esp. in human p53 gene, to identify strains of microorganisms and
XX viruses
XX
XX Example 33; Page 306; 43pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
XX selected from the group consisting of Cleavage (RPM) BN enzyme,
XX *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
XX polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
XX Rad1/Rad10 complex. The nucleic acid substrate is preferably an
XX oligonucleotide containing a human p53 gene sequence or
XX alternatively, microbial gene sequences. Cleavage products are

```
CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (wild type) and AAT29125-26
CC (mutant sequences).
XX
XX Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 tacgagcttcgatgaacc 20
        |||||||
Db      296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
XX AAT29124;
AC
AC AAT29125;
AC
AC AAT29125;
AC
DT 02-DEC-1996 (first entry)
DT
XX
XX rpoB gene fragment from Mycobacterium tuberculosis.
DE
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO9615267-A1.
XX
XX 23-MAY-1996.
XX
XX 09-NOV-1995; 95MO-US14673.
XX
XX 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
PI
XX
XX WPI; 1996-259862/26.
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
XX Example 33; Page 305; 433pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are
```

```
CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (wild type) and AAT29125-26
CC (mutant sequences).
XX
XX Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 tacgagcttcgatgaacc 20
        |||||||
Db      296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
XX AAT29125;
AC
AC AAT29125;
AC
AC AAT29125;
AC
DT 02-DEC-1996 (first entry)
DT
XX
XX rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
DE
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO9615267-A1.
XX
XX 23-MAY-1996.
XX
XX 09-NOV-1995; 95MO-US14673.
XX
XX 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
PI
XX
XX WPI; 1996-259862/26.
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
XX Example 33; Page 306; 433pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are
```

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGCGCTTCGATGAACCC 277

RESULT 8
AAT09676/c
ID AAT09676 standard; DNA: 970 BP.

XX AAT09676;

DT 15-OCT-1996 (first entry)

XX Mycobacterium tuberculosis rpoB gene DNA sequence.

XX Tuberculosis: disease diagnosis; oligonucleotide: DNA primer; PCR;
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.

XX Mycobacterium tuberculosis.

XX Location/Qualifiers

FT primer_bind

FT 10..27 /tag- a /note- "primer FENLEF"

FT primer_bind

FT 226..243 /tag- b /note- "primer DDIDL"

FT primer_bind

FT 226..240 /tag- c /note- "primer DDIDL"

FT primer_bind

FT 338..364 /tag- d /note- "primer rpo95"

FT primer_bind

FT 348..373 /tag- e /note- "primer rpo105"

FT primer_bind

FT 354..373 /tag- f /note- "primer KY290"

FT primer_bind

FT 372..373 /tag- g /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 433..434 /tag- h /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 438 /tag- i /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 468..469 /tag- j /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 486 /tag- k /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT primer_bind

FT /tag- k /note- "M. tuberculosis signature nucleotide"

FT misc_feature

FT 501 /tag- l /note- "M. tuberculosis signature nucleotide"

FT misc_feature

FT 516 /tag- m /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 516..535 /tag- n /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 525 /tag- o /note- "M. tuberculosis signature nucleotide"

FT misc_feature

FT 525 /tag- p /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 525..541 /tag- q /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 536..562 /tag- r /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 640..666 /tag- s /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- t /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- u /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- v /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- w /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- x /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- y /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- z /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- aa /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ab /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ac /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ad /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ae /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- af /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ag /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ah /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ai /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- aj /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ak /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- al /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- am /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- an /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ao /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- ap /note- "M. tuberculosis signature nucleotide"

FT primer_bind

FT 952..966 /tag- aq /note- "M. tuberculosis signature nucleotide"

FT primer_bind

RESULT 9
AAH51976/C
ID AAH51976 standard; DNA: 3519 BP.
XX
AC AAH51976;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KW Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM;
XX
DR WPI: 2001-329193/34.
DR P-PSDB: MAG81125.
XX
PT Identifying nucleotide or polypeptide sequence for use as drug target.
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure; Page 68-69; 207pp; English.
XX
CC This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins MAG81096 - MAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 1529 TACGGCGCTTCGATGAACCC 1510

RESULT 10
AAH02079/C
ID AAH02079 standard; DNA: 3534 BP.
XX
AC AAH02079;
XX
DT 24-JUL-2001 (first entry)

XX
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KW Species specific; genus specific; family specific; probe; detection;
KW identification; algal; archaeal; bacterial; fungal; parasitica;
KW microorganism; diagnosis; translation elongation factor Tu; toxin;
KW translation elongation factor G; RecA recombinase; resistance;
KW catalytic subunit of proton-translocating ATPase; antimicrobial;
KW vaccine; primer; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Ploard FJ, Roy PH;
XX
DR WPI: 2001-245006/25.
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitica species in a test sample -
XX
PS Disclosure; Page 1478-1479; 1580pp; English.
XX
CC The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitica species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (1) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 1547 TACGGCGCTTCGATGAACCC 1528

RESULT 11

```
AAA74651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651:
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US50377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
XX
PS Example 1: Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
   |||||||
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 12
AAA89994/C
ID AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994:
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
```

```
PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PR 22-APR-1999; 99US-0236894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
XX
PS Example 1: Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;
```

```
Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
   |||||||
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 13
AAT12096
ID AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096:
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinx L, Portaeis F;
```

```

PI Rosau R;
XX
XX WPI: 1996-040250/04.
DR
XX Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
XX Claim 22; Page 39; 69pp; English.
XX
XX The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC interpreting the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
XX Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;
SQ
Query Match 95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcggttcgatgaacc 19
Db 1 tacggcggttcgatgaacc 19
|||||
RESULT 14
AA051532/C
ID AA051532 standard; DNA; 3447 BP.
XX
XX AA051532;
AC
XX 17-MAY-1994 (first entry)
DT
XX
XX M. leprae rpoB gene.
DE
XX
XX rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
KW
XX
XX Mycobacterium leprae.
OS
XX
XX Key location/Qualifiers
FH CDS 1..3447
FT /*tag= a
FT /note= "rifampicin-sensitive; in resistant
FT strains the Ser codon (TCG at
FT nucleotides 1273-1275) is often mutated
FT to a Phe, Met or esp. Leu codon"
XX
XX W09322454-A.
PN
XX
XX 11-NOV-1993.
PD
XX
XX 30-APR-1993; 93WC-EP01063.
PE
XX
XX 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0815940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
XX (ASST-) ASSISTANCE PUBLIQUE.
PA (INSP) INST PASTEUR.
PA (MEDT-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.

```

```

XX Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
XX WPI: 1993-368812/46.
DR
XX P-PSDB; AAR43671.
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Fig 12; 97pp; English.
XX
XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
XX Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;
SQ
Query Match 92.0%; Score 18.4; DB 14; Length 3447;
Best Local Similarity 95.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 tacggcggttcgatgaacc 20
Db 1454 TACGGTGTTCGATGACCC 1435
|||||
RESULT 15
AAS1357/C
ID AAS1357 standard; DNA; 3474 BP.
XX
XX AAS1357;
AC
XX 13-FEB-2002 (first entry)
DT
XX
XX Enterococcus faecalis DNA for cellular proliferation protein #134.
DE
XX
XX Antisense; ds; prokaryotic cellular proliferation gene;
KM antibiotic; antibacterial; drug design.
KW
XX
XX Enterococcus faecalis.
OS
XX
XX W0200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US09180.
PE
XX
XX 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELITR-) ELITRA PHARM INC.
PA
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI: 2001-611495/70.
DR
XX P-PSDB; AAO33498.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Claim 27; Seq ID No 3939; 511pp; English.

```

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
CC
SQ Sequence 3474 BP: 1074 A; 691 C; 776 G; 933 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 3474;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 [tacggcggttcgatgaacc](#) 20
|||
Db 1652 [TAAGCGGTTTCGATGAACC](#) 1633

Search completed: August 7, 2002, 22:04:01
Job time: 8061 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:37 ; Search time 2167.9 Seconds

(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 1
Sequence: 1 tacgcgcgttcgatgaacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Genembl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_srs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mnu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_srs: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_in: *
32: em_htg_other: *
33: em_htg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
------------	-------	-------	--------	----	----	-------------

C	1	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448 Sequence
C	3	20	100.0	620	6	AR062056	AR062056 Sequence
C	4	20	100.0	620	6	AR062057	AR062057 Sequence
C	5	20	100.0	620	6	AR062058	AR062058 Sequence
C	6	20	100.0	620	6	AR062059	AR062059 Sequence
C	7	20	100.0	620	6	AR062060	AR062060 Sequence
C	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AF060353	AF060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	I50706	I50706 Sequence 1
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MSGRIFRNAP	L27989 Mycobacteri
C	14	20	100.0	5084	1	MSGRIFRNAP	AE006964 Mycobacte
C	15	20	100.0	19352	1	AE006964	295972 Mycobacteri
C	16	20	100.0	19770	1	MTC1376	AF060295 Mycobacte
C	17	18.4	92.0	626	1	AF060295	AF060295 Mycobacte
C	18	18.4	92.0	703	1	AF060349	AF060349 Mycobacte
C	19	18.4	92.0	705	1	AF060279	AF060279 Mycobacte
C	20	18.4	92.0	705	1	AF060290	AF060290 Mycobacte
C	21	18.4	92.0	705	1	AF060293	AF060293 Mycobacte
C	22	18.4	92.0	705	1	AF060297	AF060297 Mycobacte
C	23	18.4	92.0	705	1	AF060299	AF060299 Mycobacte
C	24	18.4	92.0	705	1	AF060300	AF060300 Mycobacte
C	25	18.4	92.0	705	1	AF060325	AF060325 Mycobacte
C	26	18.4	92.0	705	1	AF060326	AF060326 Mycobacte
C	27	18.4	92.0	705	1	AF060327	AF060327 Mycobacte
C	28	18.4	92.0	705	1	AF060328	AF060328 Mycobacte
C	29	18.4	92.0	705	1	AF060329	AF060329 Mycobacte
C	30	18.4	92.0	705	1	AF060331	AF060331 Mycobacte
C	31	18.4	92.0	705	1	AF060351	AF060351 Mycobacte
C	32	18.4	92.0	705	1	AF060356	AF060356 Mycobacte
C	33	18.4	92.0	3316	1	AF172323	AF172323 Bacillus
C	34	18.4	92.0	3447	6	AR067447	AR067447 Sequence
C	35	18.4	92.0	37617	1	MLB1790G	214314 M. lepreae ge
C	36	18.4	92.0	348950	1	MEPRN7	AE007977 Agrobacte
C	37	17.4	87.0	10909	1	AE007977	AE007977 Agrobacte
C	38	17.4	87.0	13047	1	AE009010	AE009010 Agrobacte
C	39	16.8	84.0	518	1	AF325874	AF325874 Staphyloc
C	40	16.8	84.0	643	1	AF060346	AF060346 Mycobacte
C	41	16.8	84.0	647	1	AF060350	AF060350 Mycobacte
C	42	16.8	84.0	652	1	AF060344	AF060344 Mycobacte
C	43	16.8	84.0	652	1	AF060364	AF060364 Mycobacte
C	44	16.8	84.0	705	1	AF060283	AF060283 Mycobacte
C	45	16.8	84.0	705	1	AF060285	AF060285 Mycobacte

ALIGNMENTS

RESULT 1
LOCUS MSGRIFRNAP/c 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit: rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 432)
Teleni, A., Imboden, P., Marchesi, F., Lowie, D., Cole, S. T.,
Colston, J., Matter, L., Schopfer, K. and Bodmer, T.
Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Agents Chemother. 341, 647-650 (1993)
FEATURES
Location/Qualifiers
1..432
/organism="Mycobacterium tuberculosis"
/strain="H37"

CDS

/db_xref="taxon:1773"
<1..>432
/codon_start=1
/transl_table=1
/product="RNA polymerase beta subunit"
/protein_id="AAB59068.1"
/db_xref="GI:149992"
/translation="GNRRRLRTVGEIIQNIRVGSRMREVRERMTTQDVEAITPQTL
INIRPVVAIKKEFGTSQSQFMDNNPLSLTHKRRLSALGPGSLSRERAGLEVRDV
HPSHYGMCPIETPECPNIGISLSVAVRVNPFGEIETPYR"
149
variation /phenotype="rifampicin resistant in association with
mutation 234 G"
188 /replace="c"
variation /phenotype="rifampicin resistant"
191 /replace="c"
variation /phenotype="rifampicin resistant in association with
mutation 203 T"
194 /replace="c"
variation /phenotype="rifampicin resistant"
203 /replace="c"
variation /phenotype="rifampicin resistant"
208..210 /replace="l"
variation /phenotype="rifampicin resistant"
232 /replace=""
variation /phenotype="rifampicin resistant"
233 /phenotype="rifampicin resistant"
232 /replace="g"
variation /phenotype="rifampicin resistant"
233 /replace="a"
variation /phenotype="rifampicin resistant"
233 /phenotype="rifampicin resistant"
233 /replace="g"
variation /phenotype="rifampicin resistant"
234 /replace="c"
variation /phenotype="rifampicin resistant"
247..248 /replace="g"
variation /phenotype="rifampicin resistant"
248 /replace="ca"
variation /phenotype="rifampicin resistant"
248 /phenotype="rifampicin resistant"
248 /replace="g"
variation /phenotype="rifampicin resistant"
254 /replace="l"
variation /phenotype="rifampicin resistant"
BASE COUNT 77 a 140 c 148 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. NO. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
AR067448/c 432 bp DNA linear PAT 29-SEP-1999
LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
ACCESSION AR067448
VERSION AR067448.1 GI:598670
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 432)
AUTHORS Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenit,A. and
Bodmer,T.
TITLE Rapid detection of antibiotic resistance in mycobacterium
tuberculosis
JOURNAL Patent: US 5851763-A 59 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..432
BASE COUNT 77 a 139 c 149 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. NO. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
AR062056/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062056
DEFINITION Sequence 135 from patent US 5843669.
ACCESSION AR062056
VERSION AR062056.1 GI:5989747
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 135 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 103 a 202 c 214 g 101 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. NO. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
AR062057/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062057
DEFINITION Sequence 136 from patent US 5843669.
ACCESSION AR062057
VERSION AR062057.1 GI:5989748
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus

Jannaschil FEN-1 endonucleases
Patent: US 5843669-A 136 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062058
DEFINITION Sequence 137 from patent US 5843669.
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
Jannaschil FEN-1 endonucleases
Patent: US 5843669-A 137 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062059
DEFINITION Sequence 138 from patent US 5843669.
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
Jannaschil FEN-1 endonucleases
Patent: US 5843669-A 138 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062060
DEFINITION Sequence 139 from patent US 5843669.
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
Jannaschil FEN-1 endonucleases
Patent: US 5843669-A 139 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062061
DEFINITION Sequence 140 from patent US 5843669.
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
Jannaschil FEN-1 endonucleases
Patent: US 5843669-A 140 01-DEC-1998;
Location/Qualifiers
1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353 AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS AF060353/c
DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,

partial cds.
AF060353
AF060353.1 GI:3133464

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 705)

REFERENCE
AUTHORS
TITLE

Glangeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
Genome Res. 8 (5), 435-448 (1998)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 705)
Glangeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
Direct Submission
Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
Location/Qualifiers

FEATURES
SOURCE

1..705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:1773"
<1..>705
/gene="rpoB"
<1..>705
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AAC38533.1"
/db_xref="GI:3133465"
/translation="QDVEAITPQTLIRPYVAIKKEFGTSIQSMQDNPLSGLT
HKRLSALPGGLSRERAGLSDVSHSHGKMPETPEGPNGILGSLSVARVP
EGFLETPEKRVADSVDEIYLTADDEDHVVQANSPIDADRFEPRVLVRKAG
EEVYPSSEVDYMYSPRQWVSATAMIPLEHDNARALMGAMQQAQVPLVASEAP
LVGTGMLRAIDAAT"

BASE COUNT 117 a 227 c 250 g 111 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 331 TACGGCGTTTCGATGACCC 312

RESULT 10
ARI49128/c 706 bp DNA linear PAT 08-AUG-2001
LOCUS ARI49128
DEFINITION Sequence 24 from patent US 6228575.
ACCESSION ARI49128
VERSION ARI49128.1 GI:15113719
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 706)
Glangeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
Ghandour,G. and Wang,C.
Chip-based species identification and phenotypic characterization
of microorganisms
Patent: US 6228575-A 24 08-MAY-2001;
Location/Qualifiers

JOURNAL
AUTHORS
TITLE
JOURNAL
FEATURES

source 1..706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGACCC 313

RESULT 11
150706/c 970 bp DNA linear PAT 07-OCT-1997
LOCUS 150706
DEFINITION Sequence 1 from patent US 5643723.
ACCESSION 150706
VERSION 150706.1 GI:2472409
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
and Whelan,A.Christian.
Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers

FEATURES
SOURCE

1..970
/organism="unknown"

BASE COUNT 182 a 302 c 330 g 156 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGACCC 652

RESULT 12
AX111339/c 3534 bp DNA linear PAT 30-APR-2001
LOCUS AX111339
DEFINITION Sequence 2072 from Patent W00123604.
ACCESSION AX111339
VERSION AX111339.1 GI:13927631
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
Bergeron,M.G., Boissnot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers

FEATURES
SOURCE

1..3534
/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"

BASE COUNT 679 a 1081 c 1188 g 586 t

ORIGIN

/translation="MLDVNPFDELRIGLATAEDIRMSYGEVKKPETINRYTLKPEKD
GLFCEKIFGPTRMCEYCGKRYKRVFGEIICERGCVEYTRAKVRERMGHLELAAPVT
HIWFKGVPSRLGYLIDLAPKDLKIIITFAAYITTSVDEMRHNEI"

BASE COUNT 969 a 1534 c 1691 g 890 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacgagcattcgatgaacc 20
|||||
Db 2611 TACGGCGTTTCGATGACCC 2592

RESULT 15
AE006964/c 19352 bp DNA linear BCT 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
DEFINITION complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS
SOURCE
ORGANISM
Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Uterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
Unpublished
2 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S.L., Delcher, A., Uterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA

TITLE
JOURNAL
FEATURES
source
1.19352
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
/db_xref="taxon:83331"
/note="clinical strain"
163..3699
/gene="MT0695"
163..3699
/gene="MT0695"
/note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
PID:149992; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK4921.1"
/db_xref="GI:13880218"
/translation="MLEGCLADSRSGKTAASPSRPOSSNNNSVYGAPNRPAPK
REPLEVGLDVOTDSFEMILIGSPRMRESAEPGDVNPVGLGEVLYELSPIDFSS
MSLSFSPDRDDWKAPYDECKDKDMYTAAPLPTAETINNTEIKSOTVFGDFPM
TEKGTIFINTEKRVVSVQLVRSPEVFDETDIKSTDTHSVKIVISRGWLEEDVK
RDIVGARDIRRRQPVVFLKALGWTSEQIVERGSEIMRSTLEKNDVTGDEALD
IYRKLRGEPPEKESAGTLENLFFKRRKDLARVGRYKYNKKLGLVGEPTSTLT
EEDVVAIIEYLRHEGOTMTVPGVEVETDDIDHFGNRRRLRTVGEONNLRG
MSMERVYRERMTODEVAITPOTLINIRPVAAIKFEFCTSOLOPMOONPLSGIT
HKRRSLALGGGSLSRERAGLEVADVHPSHIGRMCPITETPGPNIGLIGLSVYARVNP

FGFTEPRKRVVGSVDEIYVLTADEEDRVVVAOANSPIDADGRFVPRVYLRKAG
EVEVPSSEVDYNDVSRQWASVATNATIPLEHDDANRALGMQAOAPLVNSEAP
LVGTGMELEAIDADVVAEESVIEVSADYITVMDNGSTRRTYRFRARNHCT
CANQCPIDVADREAGQVADGPTDGEVALKLNILVIMPEGNINYEADAILNSR
LVDEEDVYLSHIEHEIDARTKLGAEIETRIDPNIIDEVLAIDEGIVAGVSE
GLIVGVYTPKRGTELPPEERELRAIFGERKAREYDPSLKVPHGESKVIIGVSE
DEDELPGAVNRLVAVVAAOKRKISDQKRLARHGNKGVICKILPVEDMADCTPD
IINTHGVPRRMNIGOLIERHLGCAISGKVKVDAAKVPDPAALPELLLEADQNALY
STPYDQAQEHLEGLSCTLPNRDGVAVADADKALPDRSGSEPPYVYVGMVMI
MKLHLVADDKIHARSTGPMITQPLGKAQFGGQFGEHECAWAOYGAAYTLOEL
LTIKSDTVGRVVKVYEAIVGENIPPEGIPESFVLLKELSLCLANEVLSDDAAIE
LREGEDEDLERAAANLGINLSRNESAVEDLA"

3744..7694
/gene="MT0696"
3744..7694
/gene="MT0696"
/note="similar to SP:P37871; identified by sequence
similarity; putative"
/codon_start=1
/transl_table=11
/product="DNA-directed RNA polymerase, beta-prime subunit"
/protein_id="AAK4922.1"
/db_xref="GI:13880219"
/translation="MLDVNPFDELRIGLATAEDIRMSYGEVKKPETINRYTLKPEKD
GLFCEKIFGPTRMCEYCGKRYKRVFGEIICERGCVEYTRAKVRERMGHLELAAPVT
HIWFKGVPSRLGYLIDLAPKDLKIIITFAAYITTSVDEMRHNEI"

3744..7694
/gene="MT0697"
3744..7694
/gene="MT0697"
/note="This region contains an authentic frame shift and
is not the result of a sequencing artifact; identified by
Glimmer2; putative; conserved hypothetical protein,
authentic frameshift"
10167..10925
/gene="MT0699"
10167..10925
/gene="MT0699"
/note="identified by match to pfam protein family HMM
pf01261"
/codon_start=1
/transl_table=11

/product="Ap endonuclease, family 2"
/protein_id="AAK4924.1"
/db_xref="GI:13880221"
/translation="MLIGSHVSPDDPLAAEAGADVQIFLGNPSKAPKPRDDAA
AKAATLPIYVHAPYLINLASANNRVHPTSKLQETCAAADIGAAYVHGSHVAD
DNDIDGFORMRALDRLTEVPEVYLENTGGDHAMRRPDTLARLMDVIGDIGICG
LDVCHTWAAAGEALTDADVRIKAITGRIDLHCNDSRREAGSGDRHNLNLSGQIDPDL
LVAAVKAAGAPVICETADQGRKDDIAFLRERTGS"
10957.11799
/gene="MT0700"
10957.11799
/gene="MT0700"
/note="similar to GB:U00012 PID:46863; identified by
sequence similarity: putative"
/codon_start=1
/transl_table=11
/product="hydrolase/esterase, putative"
/protein_id="AAK4925.1"
/db_xref="GI:13880222"
/translation="MLRRVALLLAAVLAFAGSGGRTLAGFGNGNSVHTLDVAGAR
SYRLKPVGLRSSAPLYVMHGGGSAKOAERSGMDELADSEKFLVAPDGYHRAN
ANGGCCGRRARREGVDICGFRAVADIANNVSIDPARVYVTGKSNKAISYTLACT
SIRALGVVSGTQIDPCQSPRPVSIHIGTADPLVRIHGGPGAGFARIDGPPVDDL
AFWRVNRGALDITTEGPTVTSATCADNRVYLLTVDDAGHRMPSFATQTLRFFA
AHRP"
11859.13487
/gene="MT0701"
11859.13487
/gene="MT0701"
/note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity:
putative"
/codon_start=1
/transl_table=11
/product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK4926.1"
/db_xref="GI:13880223"
/translation="MSDTHTVTVNOVPLENNVPASSPVLIETALIOEGGOMGLDEVNEV
GATSSAQOQRMGELADNRPIILHTHDVGYRVDEYVDPAYHELMRTAITHGHNAP
WADDRPGAHVYRAKTSVYVEBGHITCISMTYAVVPALRYNSELAYIEPLTSREY
DPELKPATKAGITAGSMTEKQSGSDVRAGITQATPNAGSISLTGHKFTSAWCD
IFVLAAQAPDGLSCFLPVLPGDTRNRMFLQRLDKLGNHNASSEVEYDGAVALV
GEEGRGVPTIIEVNLRLDCALGSATSMRTGLTRAVHQAHRKAFGAYLIDPLAME
VLADIAVEAEATIVAMMAGATDNAAVGNETELRLRIGLAAKAYWCKRSTHAAE
ALRGIGNGYVEDSGMPRLYREAPLMGIMWGSNSALDILRAMATRPACVEVLEDEL
ARSGODPRLDGVERLRFOLGDLDTIGYRARKTAEDICLALGSLVVRHGRPAVAAE
FLATRLGGQMGAGTGPAGLDLAPILERALVKG"
13498.14436
/gene="MT0702"
13498.14436
/gene="MT0702"
/note="similar to GP:3885480; identified by sequence
similarity: putative"
/codon_start=1
/transl_table=11
/product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK4927.1"
/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKTMYEVTGRIARTFNRPEKGNAIADTPL
ELSLVERADLDGVHVLIVSGREGFCAGFDSLVAEGSSSTGGAGAYOGTVLDGKT
QAVNHLPNQPMIDIDYKMSRFYRGFASLMHADKPTVYKIHGCVAGAGTIDIALHDO
VIAAADAKIGYPTPRVWGVPAAGLMAHRLGDBAKRLFTGDCITGAQAAEWGLAVEA
PEPADLDETERLVARIATLALPVNOLIMVKLALNSALLQCGVATSRMSTYFDGAARRH
PEGHAFVADAVEHGFDAVRDEPFGDYGRQASRV"
14439.15161
/gene="MT0703"
14439.15161
/gene="MT0703"
/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=11
/product="hypothetical protein"

Query Match 100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcglttcgataaaccc 20
|||||
Db 1709 TACGGCGTTTCGATGAACCC 1690

Search completed: August 7, 2002, 21:51:38
Job time: 23873 sec

Thu Aug 8 09:35:12 2002

us-09-786-105-2.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 15:14:05 : Search time 146.61 Seconds
(Without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20

Sequence: 1 tacgtcgcgcgcgcgcgcgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	4	US-08-750-088A-70	Sequence 70, Appl
2	20	100.0	306	4	US-09-147-935A-2	Sequence 2, Appl
3	20	100.0	306	4	US-09-147-935A-6	Sequence 6, Appl
4	20	100.0	306	4	US-09-147-935A-7	Sequence 7, Appl
5	20	100.0	306	4	US-09-147-935A-41	Sequence 41, Appl
6	20	100.0	306	4	US-09-147-935A-50	Sequence 50, Appl
7	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
8	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
9	20	100.0	970	1	US-08-250-030-1	Sequence 1, Appl
10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appl
11	19	95.0	306	4	US-09-147-935A-44	Sequence 44, Appl
12	18.4	92.0	25	4	US-08-750-088A-30	Sequence 30, Appl
13	18.4	92.0	306	4	US-09-147-935A-4	Sequence 4, Appl
14	18.4	92.0	306	4	US-09-147-935A-9	Sequence 9, Appl
15	18.4	92.0	306	4	US-09-147-935A-10	Sequence 10, Appl
16	18.4	92.0	306	4	US-09-147-935A-20	Sequence 20, Appl
17	18.4	92.0	306	4	US-09-147-935A-23	Sequence 23, Appl
18	18.4	92.0	306	4	US-09-147-935A-45	Sequence 45, Appl
19	17.4	87.0	306	4	US-09-147-935A-13	Sequence 13, Appl
20	17.4	87.0	306	4	US-09-147-935A-16	Sequence 16, Appl
21	17.4	87.0	306	4	US-09-147-935A-25	Sequence 25, Appl
22	17.4	87.0	306	4	US-09-147-935A-31	Sequence 31, Appl
23	17.4	87.0	306	4	US-09-147-935A-39	Sequence 39, Appl
24	17.4	87.0	306	4	US-09-147-935A-43	Sequence 43, Appl
25	17.4	87.0	306	4	US-09-147-935A-46	Sequence 46, Appl
26	17.4	87.0	306	4	US-09-147-935A-47	Sequence 47, Appl
27	16.8	84.0	306	4	US-09-147-935A-1	Sequence 1, Appl

28	16.8	84.0	306	4	US-09-147-935A-8	Sequence 8, Appl
29	15.8	79.0	306	4	US-09-147-935A-5	Sequence 5, Appl
30	15.8	79.0	306	4	US-09-147-935A-12	Sequence 12, Appl
31	15.8	79.0	306	4	US-09-147-935A-14	Sequence 14, Appl
32	15.8	79.0	306	4	US-09-147-935A-15	Sequence 15, Appl
33	15.8	79.0	306	4	US-09-147-935A-17	Sequence 17, Appl
34	15.8	79.0	306	4	US-09-147-935A-18	Sequence 18, Appl
35	15.8	79.0	306	4	US-09-147-935A-19	Sequence 19, Appl
36	15.8	79.0	306	4	US-09-147-935A-21	Sequence 21, Appl
37	15.8	79.0	306	4	US-09-147-935A-24	Sequence 24, Appl
38	15.8	79.0	306	4	US-09-147-935A-26	Sequence 26, Appl
39	15.8	79.0	306	4	US-09-147-935A-29	Sequence 29, Appl
40	15.8	79.0	306	4	US-09-147-935A-30	Sequence 30, Appl
41	15.8	79.0	306	4	US-09-147-935A-32	Sequence 32, Appl
42	15.8	79.0	306	4	US-09-147-935A-34	Sequence 34, Appl
43	15.8	79.0	306	4	US-09-147-935A-35	Sequence 35, Appl
44	15.8	79.0	306	4	US-09-147-935A-36	Sequence 36, Appl
45	15.8	79.0	306	4	US-09-147-935A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
: Sequence 70, Application US/08750088A
: Patent No. 6329138
: GENERAL INFORMATION:
: APPLICANT: DE BEENHOWER, HANS
: APPLICANT: PORTAELS, FRAN OISE
: APPLICANT: MACHTELINCKX, LIEVE
: APPLICANT: JANNES, GEERT
: APPLICANT: ROSSAU, RUDI
: TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
: TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: US
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/750,088A
: FILING DATE: 21-FEB-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLDSTEIN, JORGE A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 1657, 0010000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 70:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-750-088A-70
Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20
|||||
Db 1 TACGTCGCGCAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20
|||||
Db 5 tacggtcgcgcagctgatcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20
|||||
Db 5 tacggtcgcgcagctgatcc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20
|||||
Db 5 tacggtcgcgcagctgatcc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20
|||||
Db 5 tacggtcgcgcagctgatcc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 50
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgcatcc 20
|||||
DB 5 tacggtcgcgcgagctgcatcc 24

RESULT 7

US-08-313-185-59
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgcgcgagctgcatcc 20

|||||
DB 18 TACGTCGCGAGCTGATCC 37

RESULT 8

US-09-082-614A-59
Sequence 59, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgcatcc 20
|||||
DB 18 TACGTCGCGAGCTGATCC 37

RESULT 9

US-08-250-030-1
Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
Resistance to Rifampin in Mycobacterial Cultures and in

```

; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-030-1

Query Match          100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgatcc 20
   ||||||||||||||||
Db 261 TACGTCGGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105MO1
```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US95-06790-1

Query Match          100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgatcc 20
   ||||||||||||||||
Db 261 TACGTCGGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/09425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 44
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium xenopl
US-09-147-935A-44

Query Match          95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 acggtcgagcgtgatcc 20
   ||||||||||||||||
Db 6 acggtcgagcgtgatcc 24

RESULT 12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
```

```

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-750-088A-30

```

```

1  APPLICANT:  KOOK, Yoon-Joon
2  APPLICANT:  KIM, Bum-Joon
3  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
4  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF IP0B GENE
5  FILE REFERENCE:  0136/0F425
6  CURRENT APPLICATION NUMBER:  US/09/147,935A
7  CURRENT FILING DATE:  1999-03-19
8  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
9  PRIOR FILING DATE:  1998-07-28
10 NUMBER OF SEQ ID NOS:  50
11 SOFTWARE:  KOPATIN 1.0
12 SEQ ID NO 9
13     LENGTH:  306
14     TYPE:  DNA
15 ORGANISM:  Mycobacterium celatum Type2
16 US-09-147-935A-9

```

Thu Aug 8 09:35:10 2002

us-09-786-105-1.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 14:53:50 ; Search time 4103.44 Seconds
(Without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20

Sequence: 1 tacgtcgcgcagctgaccc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
EST:
1: em_estdb:*
2: em_estdb:*
3: em_estdb:*
4: em_estdb:*
5: em_estdb:*
6: em_estdb:*
7: em_estdb:*
8: em_estdb:*
9: em_estdb:*
10: em_estdb:*
11: em_estdb:*
12: em_estdb:*
13: em_estdb:*
14: em_estdb:*
15: em_estdb:*
16: em_estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	130	10	BM397871 5009-0-38
2	18.4	92.0	132	10	BM396091 5009-0-17
3	18.4	92.0	134	10	BM398255 5009-0-42
4	17.4	87.0	984	12	CNS01G72
5	17.4	85.0	422	10	BE443802 WHE1122.B
6	17.4	85.0	544	10	BE445100 WHE1132.H
7	17.4	85.0	558	10	BE444713 WHE1137.H
8	17.4	85.0	610	9	BE195103 HVSME008
9	17.4	85.0	658	10	BE442518 WHE1101.H
10	16.8	84.0	419	10	BG299722 HVSME002
11	16.8	84.0	419	10	B1188703 d2e05f.t
12	16.8	84.0	606	10	B1981973 fu53f08.y
13	16.8	84.0	640	10	B1888442 zF637-2.0
14	16.4	82.0	232	9	AM502654 UI-HF-BRO
15	16.4	82.0	338	9	AM501791 UI-HF-BRO
16	16.4	82.0	402	9	BE101908 UI-R-B01
17	16.4	82.0	460	9	AM502300 UI-HF-BRO

18	16.4	82.0	470	9	AM502130	AM502130 UI-HF-BRO
19	16.4	82.0	586	10	BM321268	BM321268 rockefell
20	16.4	82.0	653	10	BM320964	BM320964 rockefell
21	16.4	82.0	712	10	BM321334	BM321334 rockefell
22	16.4	82.0	899	10	BM320891	BM320891 rockefell
23	16.4	82.0	708	10	BE585978	BE585978 Est#7PT7-
24	15.8	79.0	197	6	BE59873	BE59873 P11.80.G0
25	15.8	79.0	197	6	BM318366	BM318366 P11.77.G0
26	15.8	79.0	315	10	BE419003	BE419003 WMR020.D1
27	15.8	79.0	360	10	BG412215	BG412215 OV2_39.CO
28	15.8	79.0	411	10	BG263401	BG263401 WHE2341.E
29	15.8	79.0	428	9	A1967080	A1967080 496021E08
30	15.8	79.0	451	10	C72862	C72862 C72862 Rice
31	15.8	79.0	461	10	C28055	C28055 C28055 Rice
32	15.8	79.0	493	9	BE215753	BE215753 HV_CEB000
33	15.8	79.0	507	6	BE599649	BE599649 P11.78.A0
34	15.8	79.0	507	10	BM318224	BM318224 P11.79.A0
35	15.8	79.0	560	10	BG411877	BG411877 OV2_39.CO
36	15.8	79.0	565	12	A2178000	A2178000 SP_0149.A
37	15.8	79.0	597	12	BH402082	BH402082 AC-ND-156
38	15.8	79.0	605	9	AL508804	AL508804 AL508804
39	15.8	79.0	672	9	BB316372	BB316372 BB316372
40	15.8	79.0	726	12	A2359615	A2359615 IM0102G02
41	15.8	79.0	740	12	BH016284	BH016284 TDCCK39TH
42	15.8	79.0	841	10	B1544719	B1544719 603242678
43	15.8	79.0	880	10	B1911230	B1911230 603062995
44	15.8	79.0	946	10	BG475629	BG475629 602520553
45	15.8	79.0	1077	12	CNS07739	AL432187 T3 end of

ALIGNMENTS

RESULT 1
BM397871/c 130 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION
5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
BM397871
VERSION
BM397871.1 GI:18197924

KEYWORDS
Tetrahymena thermophila.
Tetrahymena thermophila.

SOURCE
Tetrahymena thermophila.
Tetrahymena thermophila.

ORGANISM
Tetrahymena thermophila.
Tetrahymena thermophila.

REFERENCE
1 (bases 1 to 130)
Turkewitz, A.P., Karier, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

AUTHORS
Turkewitz, A.P., Karier, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel, J., and Klobutcher, L.

TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL
Unpublished (2002)

COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu

FEATURES
source
Seq primer: T3.

Location/Qualifiers
1..130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
26 a 41 c 44 g 18 t 1 others

ORIGIN

Query Match 92.0% Score 18.4; DB 10; Length 130;

Best Local Similarity 95.0%; Pred. No. 1.7e+02;

	Matches	19; Conservative	0; Mismatches	1; Indels	0; Gaps
Qy	1	tacggtcgagcagctgac	20		
	111				
Db	94	TACCGTCGGCGAGCTGATCC	75		

RESULT	2			
BM396091/c				
LOCUS	BM396091	132 bp	mRNA	linear
DEFINITION	5009-0-17-B01.t.1 Chlcoat/Turkewitz cDNA (large fraction)			
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.			
VERSION	BM396091			
KEYWORDS	BM396091.1	GI:18196144		
SOURCE	EST.			
ORGANISM	Tetrahymena thermophila.			
	Tetrahymena thermophila.			

REFERENCE	1 (bases 1 to 132)
AUTHORS	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
TITLE	EST from <i>Tetrahymena thermophila</i> , strain CU428.1, growing cells
JOURNAL	Unpublished (2002)
COMMENT	Contact: Turkewitz AP

FEATURES	Location/Qualifiers
Source	1 123

```

/organism="Tetrahymena thermophila"
/strain="CD428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      27 a      42 c      44 g      19 t
ORIGIN

```

Query Match	92.0%	Score 18.4	DB 10	Length 132
Best Local Similarity	95.0%	Pred. No. 1.7e+02		
Matches 19, Conservative	0	Mismatches 1	Indels 0	Gaps 0

```

OY      1  tacggtcgcgagctgatcc 20
          ||| ||||| ||||| |||
Db      96  TACCGTCGGCGAGCTGATCC 77

```

RESULT	3			
LOCUS	BM398255/c			
DEFINITION	BM398255	134 bp	mRNA	linear
ACCESSION	5009-0-42-H08.t.1	Chilcoat/Turkewitz cDNA (large fraction)		
		Tetrahymena thermophila cDNA, mRNA sequence.		

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 124)

University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel.: 773 702 4374
Fax: 773 702 3172
Email: apturkewendwardy.uchicago.edu
Seq primer: T3.

FEATURES	source
Location/Qualifiers	1. .134
/organism="Tetrahymena thermophila"	
/strain="Gua28.1"	
/db_xref="taxon:5911"	
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"	
/note="vector: BluescriptpZ SK+; details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."	
BASE COUNT	26 a 44 c 46 g 18 t
ORIGIN	

Query Match	92.0%;	Score 18.4;	DB 10;	Length 134;
Best Local Similarity	95.0%;	Pred. No. 1.7e+02;		
Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1  tacggtcggcgagctgatcc 20
          ||| ||||| ||||| |||
Db      98  TACCGTCGGCGAGCTGATCC 79
```

Accession	LOCUS	DEFINITION	LOCUS	DEFINITION
CNS01GJZ/c	CNS01GJZ	984 bp DNA	linear	GSS 01-JUN-2001
CNS01GJZ	Anopheles gambiae GSS T7	end of clone 06016	of Nordeamel library	from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.

REFERENCE 1 (bases 1 to 984)

TITLE Direct Submission
JOURNAL Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
Web : www.genoscope.cns.fr)
2 (b) (c) (d) (e) (f) (g) (h) (i) (j) (k) (l) (m) (n) (o) (p) (q) (r) (s) (t) (u) (v) (w) (x) (y) (z) (aa) (ab) (ac) (ad) (ae) (af) (ag) (ah) (ai) (aj) (ak) (al) (am) (an) (ao) (ap) (aq) (ar) (as) (at) (au) (av) (aw) (ax) (ay) (az) (ba) (bb) (bc) (bd) (be) (bf) (bg) (bh) (bi) (bj) (bk) (bl) (bm) (bn) (bo) (bp) (bq) (br) (bs) (bt) (bu) (bv) (bw) (bx) (by) (bz) (ca) (cb) (cc) (cd) (ce) (cf) (cg) (ch) (ci) (cj) (ck) (cl) (cm) (cn) (co) (cp) (cq) (cr) (cs) (ct) (cu) (cv) (cw) (cx) (cy) (cz) (da) (db) (dc) (dd) (de) (df) (dg) (dh) (di) (dj) (dk) (dl) (dm) (dn) (do) (dp) (dq) (dr) (ds) (dt) (du) (dv) (dw) (dx) (dy) (dz) (ea) (eb) (ec) (ed) (ee) (ef) (eg) (eh) (ei) (ej) (ek) (el) (em) (en) (eo) (ep) (eq) (er) (es) (et) (eu) (ev) (ew) (ex) (ey) (ez) (fa) (fb) (fc) (fd) (fe) (ff) (fg) (fh) (fi) (fj) (fk) (fl) (fm) (fn) (fo) (fp) (fq) (fr) (fs) (ft) (fu) (fv) (fw) (fx) (fy) (fz) (ga) (gb) (gc) (gd) (ge) (gf) (gg) (gh) (gi) (gj) (gk) (gl) (gm) (gn) (go) (gp) (gq) (gr) (gs) (gt) (gu) (gv) (gw) (gx) (gy) (gz) (ha) (hb) (hc) (hd) (he) (hf) (hg) (hh) (hi) (hj) (hk) (hl) (hm) (hn) (ho) (hp) (hq) (hr) (hs) (ht) (hu) (hv) (hw) (hx) (hy) (hz) (ia) (ib) (ic) (id) (ie) (if) (ig) (ih) (ii) (ij) (ik) (il) (im) (in) (io) (ip) (iq) (ir) (is) (it) (iu) (iv) (iw) (ix) (iy) (iz) (ja) (jb) (jc) (jd) (je) (jf) (jg) (jh) (ji) (jj) (jk) (jl) (jm) (jn) (jo) (jp) (jq) (jr) (js) (jt) (ju) (jv) (jw) (jx) (jy) (jz) (ka) (kb) (kc) (kd) (ke) (kf) (kg) (kh) (ki) (kj) (kk) (kl) (km) (kn) (ko) (kp) (kq) (kr) (ks) (kt) (ku) (kv) (kw) (kx) (ky) (kz) (la) (lb) (lc) (ld) (le) (lf) (lg) (lh) (li) (lj) (lk) (ll) (lm) (ln) (lo) (lp) (lq) (lr) (ls) (lt) (lu) (lv) (lw) (lx) (ly) (lz) (ma) (mb) (mc) (md) (me) (mf) (mg) (mh) (mi) (mj) (mk) (ml) (mm) (mn) (mo) (mp) (mq) (mr) (ms) (mt) (mu) (mv) (mw) (mx) (my) (mz) (na) (nb) (nc) (nd) (ne) (nf) (ng) (nh) (ni) (nj) (nk) (nl) (nm) (nn) (no) (np) (nq) (nr) (ns) (nt) (nu) (nv) (nw) (nx) (ny) (nz) (oa) (ob) (oc) (od) (oe) (of) (og) (oh) (oi) (oj) (ok) (ol) (om) (on) (oo) (op) (oq) (or) (os) (ot) (ou) (ov) (ow) (ox) (oy) (oz) (pa) (pb) (pc) (pd) (pe) (pf) (pg) (ph) (pi) (pj) (pk) (pl) (pm) (pn) (po) (pp) (pq) (pr) (ps) (pt) (pu) (pv) (pw) (px) (py) (pz) (qa) (qb) (qc) (qd) (qe) (qf) (qg) (qh) (qi) (qj) (qk) (ql) (qm) (qn) (qo) (qp) (qq) (qr) (qs) (qt) (qu) (qv) (qw) (qx) (qy) (qz) (ra) (rb) (rc) (rd) (re) (rf) (rg) (rh) (ri) (rj) (rk) (rl) (rm) (rn) (ro) (rp) (rq) (rr) (rs) (rt) (ru) (rv) (rw) (rx) (ry) (rz) (sa) (sb) (sc) (sd) (se) (sf) (sg) (sh) (si) (sj) (sk) (sl) (sm) (sn) (so) (sp) (sq) (sr) (ss) (st) (su) (sv) (sw) (sx) (sy) (sz) (ta) (tb) (tc) (td) (te) (tf) (tg) (th) (ti) (tj) (tk) (tl) (tm) (tn) (to) (tp) (tq) (tr) (ts) (tt) (tu) (tv) (tw) (tx) (ty) (tz) (ua) (ub) (uc) (ud) (ue) (uf) (ug) (uh) (ui) (uj) (uk) (ul) (um) (un) (uo) (up) (uq) (ur) (us) (ut) (uu) (uv) (uw) (ux) (uy) (uz) (va) (vb) (vc) (vd) (ve) (vf) (vg) (vh) (vi) (vj) (vk) (vl) (vm) (vn) (vo) (vp) (vq) (vr) (vs) (vt) (vu) (vv) (vw) (vx) (vy) (vz) (wa) (wb) (wc) (wd) (we) (wf) (wg) (wh) (wi) (wj) (wk) (wl) (wm) (wn) (wo) (wp) (wq) (wr) (ws) (wt) (wu) (wv) (ww) (wx) (wy) (wz) (xa) (xb) (xc) (xd) (xe) (xf) (xg) (xh) (xi) (xj) (xk) (xl) (xm) (xn) (xo) (xp) (xq) (xr) (xs) (xt) (xu) (xv) (xw) (xx) (xy) (xz) (ya) (yb) (yc) (yd) (ye) (yf) (yg) (yh) (yi) (yj) (yk) (yl) (ym) (yn) (yo) (yp) (yq) (yr) (ys) (yt) (yu) (yv) (yw) (yx) (yz) (za) (zb) (zc) (zd) (ze) (zf) (zg) (zh) (zi) (zj) (zk) (zl) (zm) (zn) (zo) (zp) (zq) (zr) (zs) (zt) (zu) (zv) (zw) (zx) (zy) (zz)

JOURNAL Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
Roux, Paris 75015, France
COMMENT This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES	source
Location/Qualifiers	1. .984
/organism="Anopheles gambiae"	
/strain="PEST"	
/db_xref="taxon:7165"	
/clone="06016"	
/clone_lib="Notredame1"	
/note="end : T7"	
BASE COUNT	272 a 236 c 241 g 232 t 3 others
ORIGIN	

Query Match	87.0%	Score 17.4	DB 12	Length 984
Best Local Similarity	94.7%	Pred. No. 7.4e+02		
Matches 18	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY 1 tacggtcgcgagctgac 19
 |||||
 Db 103 TACGTCGCGAGCTGATTC 85

RESULT 5
 BE443802 422 bp mRNA linear EST 25-JUL-2000
 LOCUS WHE1122_B06_C12S wheat etiolated seedling root normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA

ACCESSION BE443802
 VERSION BE443802
 KEYWORDS GI:9443341
 SOURCE EST
 ORGANISM bread wheat.
 Triticum aestivum

REFERENCE
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Trilicaceae; Triticum.
 1 (bases 1 to 422)
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.
 Location/Qualifiers

FEATURES
 source
 1..422
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1122_B06_C12"
 /clone_11b="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluescript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
 ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
 Best Local Similarity 100.0%; Pred. NO. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ggtcgcgagctgac 20
 |||||

Db 86 GCTCGCGAGCTGATTC 102

RESULT 6
 BE445100 544 bp mRNA linear EST 25-JUL-2000
 LOCUS WHE1132_H08_P16S wheat etiolated seedling root normalized cDNA
 DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA

ACCESSION BE445100
 VERSION BE445100
 KEYWORDS GI:9444655
 SOURCE EST
 ORGANISM bread wheat.
 Triticum aestivum

REFERENCE
 AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Trilicaceae; Triticum.
 1 (bases 1 to 544)
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.
 Location/Qualifiers

FEATURES
 source
 1..544
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1132_H08_P16"
 /clone_11b="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluescript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
 ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
 Best Local Similarity 100.0%; Pred. NO. 9.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ggtcgcgagctgac 20
 |||||
 Db 512 GCTCGCGAGCTGATTC 528

RESULT 7
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS BE444713
DEFINITION WHE1137_H03_005ZS Wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713
VERSION BE444713
KEYWORDS GI:9444264
SOURCE
ORGANISM
Triticum aestivum
bread wheat.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 558)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
, P.S., Hala, C.C., Kang, Y., Iazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
JOURNAL
COMMENT
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
Location/Qualifiers

FEATURES

Source

1..558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/note="stage=Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI. Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT

122 a 180 c 134 g 122 t

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 ggtcggcagctgaccc 20
|||||
Db 514 gctcggcagctgaccc 530

RESULT 8

BE195103
LOCUS BE195103
DEFINITION
HVSMEH0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0088E21f,
mRNA sequence.
ACCESSION BE195103
VERSION BE195103
KEYWORDS GI:16321083
SOURCE
ORGANISM
Hordeum vulgare
barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 238
Seq primer: AATTAACCTCAGTAAGGG
High quality sequence stop: 563.
Location/Qualifiers

FEATURES

Source

1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI.
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinholz A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT

127 a 203 c 158 g 120 t 2 others

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgcgcgcgcgcgc 20
 DB 499 GGTCCGCCGAGCTGATCC 515

RESULT 9
 BE442518 658 bp mRNA linear EST 25-JUL-2000
 LOCUS BE442518
 DEFINITION library Triticum aestivum cDNA clone WHE1101_H10_019, mRNA

ACCESSION BE442518
 VERSION BE442518
 KEYWORDS EST
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 658)
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,
 P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.

FEATURES

source
 1. 658
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1101_H10_019"
 /clone.lib="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluscript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluscript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 144 a 209 c 165 g 140 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 658;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgcgcgcgcgcgc 20

DB 512 GGTCCGCCGAGCTGATCC 528

RESULT 10
 BG299722 828 bp mRNA linear EST 17-OCT-2001
 LOCUS HVSME0021120f Hordeum vulgare seedling shoot EST library
 DEFINITION HVCNMA0001 (Cold stress) Hordeum vulgare cDNA clone HVSME0021120f,
 mRNA sequence.

ACCESSION BG299722
 VERSION BG299722
 KEYWORDS EST
 SOURCE barley.
 ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 828)
 Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu,
 Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.,
 Fenton,R.D. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library
 Unpublished (2001)

TITLE
 JOURNAL
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293

Email: rwing@clemson.edu
 Total hg bases = 574
 Seq primer: AATTAACTCCTCACTAAAGG
 High quality sequence stop: 643.

FEATURES

source
 1. 828
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME0021120f"
 /clone.lib="Hordeum vulgare seedling shoot EST library
 HVCNMA0001 (Cold stress)"
 /tissue_type="Seedling shoot"
 /lab_host="TJC121"
 /note="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give pluscript SK(-) cDNA
 phagemids. These steps were performed in the TJ Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g9pages/pgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gtcgcgcagactgcatcc 20
|||||
DB 500 GGTCGCGAGCTGATCC 516

RESULT 11
B1188703/c 419 bp mRNA linear EST 10-JUL-2001
LOCUS d2e05fs.r1 Fusarium sporotrichioides Tr1 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
sequence.

ACCESSION B1188703
VERSION B1188703.1 GI:14662382
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
REFERENCE Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
M., and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other-ESTs: d2e05fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contract Dr. Marlan Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
73 2.2 g117799258|emb|CAB90 (AL355752) putative integral
membrane prote
Seg primer: T3
High quality sequence stop: 107.
Location/Qualifiers
1..419
/organism="Fusarium sporotrichioides"
/strain="Tr1 10"
/db_xref="taxon:5514"
/clone_id="d2e05fs"
/clone_lib="Fusarium sporotrichioides Tr1 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 117 a 106 c 117 g 79 t
ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 419;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tacggtcgcgcagctgcatcc 20
|||||
DB 114 TACGCTCAGCGAGCTGATCC 95

RESULT 12
B1981973/c 606 bp mRNA linear EST 24-OCT-2001
LOCUS fu33f08.v1 zebrafish adult brain Danio rerio cDNA clone 533151 5'
DEFINITION similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN;; mRNA sequence.

ACCESSION B1981973
VERSION B1981973.1 GI:16371108
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
REFERENCE Clark,M., Johnson,S.L., Lebrach,H., Lee,R., Li,F., Marra,M., Eddy
S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
'K., Steptoe,M., Rheising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Mashu zebrafish EST Project 1998
Unpublished (1998)
Other-ESTs: fu33f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone Distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
ResourcenZentrumPrimateDataBank, Berlin, Germany (web address:
www.rzpdp.de)
High quality sequence stop: 446.
Location/Qualifiers
1..606
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_id="533151"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/note="Vector: pZIRLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZIRLOX. Mass
excision of the cDNA library was performed to yield
pZIRLOX plasmids. Insert check was done in original
library."
BASE COUNT 209 a 133 c 139 g 125 t
ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 606;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 tacggtcgcgcagctgcatcc 20
|||||
DB 452 TACGCTCAGCGAGCTGTAC 433

RESULT 13
B1888442/c 640 bp mRNA linear EST 12-OCT-2001
LOCUS zF637-2-000197 zebrafish shield stage whole embryo cDNA library
DEFINITION MPMGP637 Danio rerio cDNA clone MPMGP637_18E17; MPMGP637E1718 5',
mRNA sequence.
ACCESSION B1888442
VERSION B1888442.1 GI:16095713
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 640)
Clark, M., Amstutz, P., Hennig, S., Johnson, S.L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
Contact: Hennig S
laboratory 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Imestr.63-73, D-14195 Berlin, Germany
Tel.: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.

FEATURES
source

Location/Qualifiers
1..640
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMP637_18E17:MPMP637E1718"
/clone_lib="Zebrafish shield stage whole embryo cDNA
library MPMP637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 blue MR"
/note="Vector: pSPori1; Site_1: NotI; Site_2: SalI;
oligo-OT-Moti primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"

BASE COUNT
ORIGIN

209 a 152 c 139 g 139 t 1 others

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 10; Length 640;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taagtcgcgcagctgacc 20
|||||
Db 541 TACGCTCGCGCTGTAC 522

RESULT 14
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM502654 292 bp mRNA linear EST 01-MAR-2000
UI-HF-BRDP-ajx-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075813 5', mRNA sequence.
AM502654
AM502654.1 GI:7117309
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 292)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..292

Query Match
Best Local Similarity 82.0%; Score 16.4; DB 9; Length 292;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acgctgcgcagctgacc 19
|||||
Db 46 ACGCTCGCGCTGTATC 63

RESULT 15
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM501791 338 bp mRNA linear EST 01-MAR-2000
UI-HF-BRDP-ajm-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075260 5', mRNA sequence.
AM501791
AM501791.1 GI:7115654
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 338)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..338
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075260"
/clone_lib="NIH_MGC_52"
/tissue_type="lymph"
/tissue_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pRT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "

BASE COUNT
ORIGIN

56 a 98 c 124 g 60 t

Query Match
82.0%; Score 16.4; DB 9; Length 338;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggtcggcgagctgac 19
|||||
Db 46 ACGGTGGGCGGTGATC 63

Search completed: August 7, 2002, 21:15:17
Job time: 2287 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 15:13:45 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacgctgcgcgcgcctcacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGR1RNAP	MSGR1RNAP
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	MTU12205 Mycobacteri
16	20	100.0	5084	1	MSGR0B	MSGR0B Mycobacteri
17	20	100.0	19352	1	AE069664	AE069664 Mycobacte
18	20	100.0	19770	1	MTC1376	MTC1376 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18.4	92.0	25	6	AA7816	AA7816 Sequence 30
22	18.4	92.0	306	1	AF057456	AF057456 Mycobacte
23	18.4	92.0	306	1	AF057459	AF057459 Mycobacte
24	18.4	92.0	306	1	AF057460	AF057460 Mycobacte
25	18.4	92.0	306	1	AF057471	AF057471 Mycobacte
26	18.4	92.0	306	1	AF057473	AF057473 Mycobacte
27	18.4	92.0	306	1	AF057496	AF057496 Corynebact
28	18.4	92.0	306	1	AF173087	AF173087 Mycobacte
29	18.4	92.0	306	6	AR157005	AR157005 Sequence
30	18.4	92.0	306	6	AR157010	AR157010 Sequence
31	18.4	92.0	306	6	AR157011	AR157011 Sequence
32	18.4	92.0	306	6	AR157021	AR157021 Sequence
33	18.4	92.0	306	6	AR157024	AR157024 Sequence
34	18.4	92.0	306	6	AR157046	AR157046 Sequence
35	18	90.0	87	6	AX050338	AX050338 Sequence
36	17.4	87.0	306	1	AF057463	AF057463 Mycobacte
37	17.4	87.0	306	1	AF057466	AF057466 Mycobacte
38	17.4	87.0	306	1	AF057475	AF057475 Mycobacte
39	17.4	87.0	306	1	AF057480	AF057480 Mycobacte
40	17.4	87.0	306	1	AF057489	AF057489 Mycobacte
41	17.4	87.0	306	1	AF057492	AF057492 Mycobacte
42	17.4	87.0	306	1	AF057494	AF057494 Rhodococc
43	17.4	87.0	306	1	AF057495	AF057495 Nocardi
44	17.4	87.0	306	1	AF173084	AF173084 Mycobacte
45	17.4	87.0	306	1	AF173086	AF173086 Mycobacte

ALIGNMENTS

RESULT 1
AF057450 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial
DEFINITION
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS
SOURCE
ORGANISM

Mycobacterium africanum.
Mycobacterium africanum
Bacteria: Firmicutes: Actinobacteria: Actinobacteriidae:
Actinomycetales: Corynebacteriales: Mycobacteriaceae:
Mycobacterium: Mycobacterium tuberculosis complex.

REFERENCE
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES
source

Location/Qualifiers
1. .306
/organism="Mycobacterium africanum"

/strain="ATCC25420"

/db_xref="ATCC:25420"

/db_xref="taxon:33894"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="A055514.1"

/db_xref="GI:5902488"

/translation="RTVGLLIONQIRVGSRMERVRMTODVEAITPQTLINIRP
VVAIRKEFFGTSOLSFMDQNNPLSGITHKRRRLSALPGLSRERAGLEVVDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagctgaccc 20
|||||
Db 5 TACGTCGCGAGCTGATCC 24

RESULT 2
LOCUS AF057451 306 bp DNA linear BCT 17-SEP-1999

DEFINITION Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057451

VERSION AF057451.1 GI:5902489

KEYWORDS Mycobacterium bovis.

SOURCE Mycobacterium bovis.

ORGANISM Mycobacterium bovis.

REFERENCE 1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Location/Qualifiers

1. .306
/organism="Mycobacterium bovis"

/strain="ATCC19210"

/db_xref="ATCC:19210"

/db_xref="taxon:1765"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

/transl_table=11
/product="RNA polymerase beta"

/protein_id="A055515.1"

/db_xref="GI:5902490"

/translation="RTVGLLIONQIRVGSRMERVRMTODVEAITPQTLINIRP
VVAIRKEFFGTSOLSFMDQNNPLSGITHKRRRLSALPGLSRERAGLEVVDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagctgaccc 20
|||||
Db 5 TACGTCGCGAGCTGATCC 24

RESULT 3
LOCUS AF057452 306 bp DNA linear BCT 17-SEP-1999

DEFINITION Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
(rpoB) gene, partial cds.

ACCESSION AF057452

VERSION AF057452

KEYWORDS Mycobacterium bovis BCG.

SOURCE Mycobacterium bovis BCG.

ORGANISM Mycobacterium bovis BCG.

REFERENCE 1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Location/Qualifiers

1. .306
/organism="Mycobacterium bovis BCG"

/strain="French 1173P2"

/db_xref="taxon:33892"

<1. .>306
/gene="rpoB"

<1. .>306
/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="A055516.1"

/db_xref="GI:5902492"

/translation="RTVGLLIONQIRVGSRMERVRMTODVEAITPQTLINIRP
VVAIRKEFFGTSOLSFMDQNNPLSGITHKRRRLSALPGLSRERAGLEVVDVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagctgaccc 20
|||||
Db 5 TACGTCGCGAGCTGATCC 24

DB 5 TACGCTCGCGAGCTGATCC 24

RESULT 4

LOCUS AF057453 306 bp DNA linear BCT 17-SEP-1999

DEFINITION Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057453

VERSION AF057453.1 GI:5902493

KEYWORDS

SOURCE Mycobacterium bovis BCG.

ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.

TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)

AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Yongsong-dong, Chongno-gu, Seoul 110-799, Korea

FEATURES

source 1..306

location/Qualifiers

1..306

/organism="Mycobacterium bovis BCG"

/strain="Tokyo 1172"

/db_xref="taxon:33892"

<1..>306

/gene="rpoB"

<1..>306

/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="AAD5517.1"

/db_xref="GI:5902494"

/translation="RTVSELIQNIIRVGSRMRERVRERMTTQDVEATTPQILNIRP VVAATKEFGTSQLSQFMDQNNPLSGTLTKRRLSALGPGGLSRERAGLEVRVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgcgagctgatcc 20

|||||

DB 5 TACGCTCGCGAGCTGATCC 24

RESULT 5

LOCUS AF057454 306 bp DNA linear BCT 08-OCT-1999

DEFINITION Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057454

VERSION AF057454.1 GI:5902495

KEYWORDS

SOURCE Mycobacterium tuberculosis.

ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.

TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

MEDLINE 99262756

PUBMED 10325313

REFERENCE 2 (bases 1 to 306)

AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Yongsong-dong, Chongno-gu, Seoul 110-799, Korea

FEATURES

source 1..306

location/Qualifiers

1..306

/organism="Mycobacterium tuberculosis"

/strain="H37Rv; ATCC27294"

/db_xref="ATCC:27294"

/db_xref="taxon:1773"

<1..>306

/gene="rpoB"

<1..>306

/gene="rpoB"

/codon_start=3

/transl_table=11

/product="RNA polymerase beta"

/protein_id="AAD5518.1"

/db_xref="GI:5902496"

/translation="RTVSELIQNIIRVGSRMRERVRERMTTQDVEATTPQILNIRP VVAATKEFGTSQLSQFMDQNNPLSGTLTKRRLSALGPGGLSRERAGLEVRVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgcgagctgatcc 20

|||||

DB 5 TACGCTCGCGAGCTGATCC 24

RESULT 6

LOCUS ARI57003 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 2 from patent US 6242584.

ACCESSION ARI57003

VERSION ARI57003.1 GI:15125707

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene

JOURNAL Patent: US 6242584-A 2 05-JUN-2001;

FEATURES

source 1..306

location/Qualifiers

1..306

/organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgcgagctgatcc 20

|||||

Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y.-H. and Kim,B.-J.
TITLE Method for identifying mycobacterial species by comparative
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgatcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 8
LOCUS ARI57008 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgatcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 9
LOCUS ARI57042 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgatcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 10
LOCUS ARI57051 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgatcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37).
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,T., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

FEATURES
source
Location/Qualifiers
1. .432
/organism="Mycobacterium tuberculosis"
/strain="H37"
/db_xref="taxon:1773"
<1. .>432
/codon_start=1
/transl_table=11
/product="RNA polymerase beta subunit"
/protein_id="AB59068.1"
/db_xref="GI:14992"
/translacion="GNRLRTVGLIQNIQVMSRMERYRRTTODVATTPQTL
INRPVVAIKEFTQSOLFQMDONNPLSLTKRRRLSALGGGSLSRERAGLEVBDV
HSHYGRMCPRIEPEGPNIGLISLVYARVNPFFIEPYR"
149
/phenotype="rifampicin resistant in association with
mutation 234 G"
/replace="c"
188
/phenotype="rifampicin resistant"
/replace="c"
191
/phenotype="rifampicin resistant in association with
mutation 203 T"
/replace="c"
194
/phenotype="rifampicin resistant"
/replace="t"
203
/phenotype="rifampicin resistant"
/replace="t"
208. .210
/phenotype="rifampicin resistant"
/replace="a"
232
/phenotype="rifampicin resistant"
/replace="g"
232
/phenotype="rifampicin resistant"
/replace="a"
233
/phenotype="rifampicin resistant"
/replace="g"
233
/phenotype="rifampicin resistant"
/replace="c"
234
/phenotype="rifampicin resistant"
/replace="g"
247. .248
/phenotype="rifampicin resistant"
/replace="ca"
248
/phenotype="rifampicin resistant"
/replace="g"
248
/phenotype="rifampicin resistant"
/replace="t"
254
/phenotype="rifampicin resistant"
/replace="c"
BASE COUNT 77 a 140 c 148 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 18 TACGCTCGCGAGCTGATCC 37

RESULT 12
AR067448
LOCUS AR067448 432 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 59 from patent US 5851763.
AR067448
VERSION AR067448.1 GI:5998670
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 432)
AUTHORS
Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
Bodmer, T.
TITLE
Rapid detection of antibiotic resistance in mycobacterium
tuberculosis
Patent: US 5851763-A 59 22-DEC-1998;
FEATURES
source
Location/Qualifiers
1. .432
/organism="unknown"
BASE COUNT 77 a 139 c 149 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 18 TACGCTCGCGAGCTGATCC 37

RESULT 13
I50706
LOCUS I50706 970 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5643723.
ACCESSION I50706
VERSION I50706.1 GI:2472409
KEYWORDS
Unknown.
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 970)
AUTHORS
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmler, T.A., Roberts, G.D.
and Whelan, A. Christian.
TITLE
Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
JOURNAL
Patent: US 5643723-A 1 01-JUL-1997;
FEATURES
source
Location/Qualifiers
1. .970
/organism="unknown"
BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 261 TACGCTCGCGAGCTGATCC 280

RESULT 14
AX111339
LOCUS AX111339 3534 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 2072 from Patent W00123604.
AX111339
VERSION AX111339.1 GI:13927631
KEYWORDS
Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
Bergeon, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J., and Roy, P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgagcagctgatcc 20
|||||
Db 1137 TACGCTCGCGAGCTGATCC 1156
RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The rpoB gene of Mycobacterium tuberculosis
Unpublished
2 (bases 1 to 3853)
Imboden, P.
Direct Submission
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
Location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
576..>3853
/gene="rpoB"
/codon_start=-1
/transl_table=11
/product="RNA-polymerase beta subunit"
/protein_id="AA020242.2"
/db_xref="GI:7144499"
/translation="MLEGCIADSRQSKTASPSPSSNNNSVPGAPNRYSAFL
REPLEVGLDVQTDSEFLICSPRMRESAERGVNPGLEVLIELSPIEDSGS
MSLSFDPREDVAPYDECKDKDMYAAPLEFVTAEPINNNGEIKSOTYVMDPFPMM
TEKGTFLNCTERVVSVLRSPGVFEDRDKSTDKLHSAVKVIBSRGAMLEFDVVK
RDVGVRIIDKRPQVTVLKAIGWTSQIVERFGSEIKRSTLEKNTVGTDEALD
ITKLRPGEPPTESAQTLELNFKEKRYDIARVGKRYKRLGLHVGEPITSTLT

EEDVVAITIELVLRHEGQTTWTVPGVEVPEVETDDIDHFGNRRRLRTVGEILQNIQIRVG
MSRMRVVRREMTQDVEAIPOTFLINRPVVAIKEPFGTSOSOPMDONNPLSGLT
HKRRSLAGGGSLRRAGLEVRRVHPSHVGRMCPIETPEGPNTIGLSISVARNP
EGFIETPYRKVYDGVSDGYIYLLADEDRRVVAQNSPIDADRFPEPRVLYRRKAS
EVERVPSSEVDYKDVSPROMVSATAMIPLEHDDANPLAGANMORQAVLVSEAP
LVYGMELRAIDAATSSQSESGVIEEVSADYIYMHONGRRYRMRKFRSHNGTC
ANOCPIVDAGRVAGOVIA DGPCITDGEMLGKNLVAIIPMEGHVYEDAIIISNRL
VEEDVLSIHIEHEIDARDTKLGAEEITRDIPNISPEVLADDERGIVRIGAEVRDG
DIIVGKVTYPRGEMETLPEERLLRAIPGEKAREVDTSLKVPBGSGKVGITGRVPSRED
EDELPAVNELVRRYVNAQKRISDGLAGRHGKGYIGKILPYEDMPLADTPYVDI
ILNTHGVPRRNNIGQIILETHLGCWAHSGMKVDAGVPMARLPLDELEQPNATVS
TPYFDGAQEAELQGLISCTLPNRDGLVDADGAMLEFDGSGEPFPYPVVGYVYM
KLHLLVYDCKIHARSTGPYMTQQPLGKKAQFGGQREGMECMAMQAYGAAYTLQELL
TIKS"
BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgagcagctgatcc 20
|||||
Db 1712 TACGCTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 21:51:37
Job time: 23872 sec

Thu Aug 8 09:35:10 2002

us-09-786-105-1.rge

Page 7

THIS PAGE IS BLANK

THIS PAGE IS BLANK

PT Probes and primers for determin. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene

XX Claim 22, Page 39, 69pp; English.

CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determin.
CC of ARS and spp. identity.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

QY Query Match

Best Local Similarity 100.0%; Score 20; DB 17; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tacggtcgcgcagctgattcc 20
1 tacggtcgcgcagctgattcc 20

RESULT 2

AAA49823 standard; DNA; 20 BP.

AC AAA49823;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

OS Mycobacterium tuberculosis.

PN MO200036142-A1.

PD 22-JUN-2000.

10-DEC-1999; 99MO-CA01177.

11-DEC-1998; 98US-0111794.

(VIST-) VISIBLE GENETICS INC.

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium
tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 4; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-associated mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

QY Query Match

Best Local Similarity 100.0%; Score 20; DB 21; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tacggtcgcgcagctgattcc 20
1 tacggtcgcgcagctgattcc 20

RESULT 3

AAA49825 standard; DNA; 20 BP.

AC AAA49825;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

OS Mycobacterium tuberculosis.

PN MO200036142-A1.

PD 22-JUN-2000.

10-DEC-1999; 99MO-CA01177.

11-DEC-1998; 98US-0111794.

(VIST-) VISIBLE GENETICS INC.

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium
tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 5; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

THIS PAGE IS BLANK

OS	Synthetic.
XX	
PN	
XX	
PD	14-DEC-1995.
XX	
PE	09-JUN-1995; 95WO-EP02230.
XX	
PR	09-JUN-1994; 94EP-0870093.
XX	
PA	(INNO-) INNOGENETICS NV.
PI	De Beenhouwer H, Jannes G, Machtelincx L, Portaeals F,
PI	Rossau R;
XX	
DR	WPI; 1996-040250/04.
XX	

THIS PAGE IS BLANK

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
PS Claim 22: Page 39: 69pp: English.

CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT2091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.

SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgattcc 20
1 tacggtcgcgagctgattcc 20

RESULT 2
ID AAA49823 standard; DNA: 20 BP.
AC AAA49823;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shupman R;

PT WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 4; 43pp: English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mba (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgagctgattcc 20
1 tacggtcgcgagctgattcc 20

RESULT 3
ID AAA49825 standard; DNA: 20 BP.
AC AAA49825;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shupman R;

PT WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 5; 43pp: English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mba (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:45 ; Search time 147.68 seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 tacggcgttcgatyacc 20

Scoring table: OLIGO_NUC
Gapex 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/1na/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/1na/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	432	2 US-08-313-185-59	Sequence 59, App1
2	20	100.0	432	3 US-09-082-614A-59	Sequence 59, App1
3	20	100.0	620	2 US-08-757-653-135	Sequence 135, App
4	20	100.0	620	2 US-08-757-653-136	Sequence 136, App
5	20	100.0	620	2 US-08-757-653-137	Sequence 137, App
6	20	100.0	620	2 US-08-757-653-138	Sequence 138, App
7	20	100.0	620	2 US-08-757-653-139	Sequence 139, App
8	20	100.0	620	2 US-08-757-653-140	Sequence 140, App
9	20	100.0	620	2 US-08-757-653-140	Sequence 140, App
10	20	100.0	970	1 US-08-250-030-1	Sequence 1, App1
11	20	100.0	970	5 PCT-US95-06790-1	Sequence 1, App1
12	19	95.0	19	4 US-08-750-088A-71	Sequence 71, App1
13	15	75.0	27	1 PCT-US95-06790-9	Sequence 9, App1
14	15	75.0	27	5 PCT-US95-06790-9	Sequence 9, App1
15	14	70.0	3447	2 US-08-313-185-57	Sequence 57, App1
16	14	70.0	3447	3 US-09-082-614A-57	Sequence 57, App1
17	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
18	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
19	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
20	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
21	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
22	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
23	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
24	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
25	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
26	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
27	13	65.0	383	3 US-08-906-769-169	Sequence 169, App

28	13	65.0	537	4 US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4 US-09-232-200-29	Sequence 29, App1
30	13	65.0	1938	4 US-09-232-197-29	Sequence 29, App1
31	13	65.0	1938	4 US-09-232-201-29	Sequence 29, App1
32	13	65.0	3000	2 US-08-896-344A-1	Sequence 1, App1
33	13	65.0	3000	4 US-09-360-682A-1	Sequence 1, App1
34	13	65.0	3217	4 US-09-232-200-64	Sequence 64, App1
35	13	65.0	3217	4 US-09-232-197-64	Sequence 64, App1
36	13	65.0	3217	4 US-08-282-696-19	Sequence 64, App1
37	13	65.0	4403765	4 US-09-103-840A-2	Sequence 2, App1
38	12	60.0	391	1 US-08-636-928-6	Sequence 6, App1
39	12	60.0	412	4 US-08-976-259-123	Sequence 13, App
40	12	60.0	645	1 US-08-459-586-19	Sequence 19, App1
41	12	60.0	645	2 US-08-282-696-19	Sequence 19, App1
42	12	60.0	648	5 PCT-US95-04648-4	Sequence 4, App1
43	12	60.0	709	1 US-08-459-586-20	Sequence 20, App1
44	12	60.0	709	2 US-08-282-696-20	Sequence 20, App1
45	12	60.0	728	4 US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Teleni, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

THIS PAGE IS BLANK

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
US-09-082-614A-59/C

Sequence 59, Application US/09082614A

Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate

APPLICANT: Cole, Stewart

APPLICANT: Young, Douglas

APPLICANT: Zhang, Ying

APPLICANT: Honore, Nadine

APPLICANT: Telenti, Amalio

TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

TITLE OF INVENTION: In Mycobacterium Tuberculosis

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,614A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/313,185

FILING DATE: 12-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356, 0068-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-082-614A-59

Query Match

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20

|||||

DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/C

Sequence 135, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:

LENGTH: 620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-135

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 620;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20

|||||

DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/C

Sequence 136, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:52 ; Search time 147.68 seconds

(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-4

Sequence: 1 tacggcgttcgatgacc 20

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents, NA: *
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCrUS.COMB.seq: *
6: /cgn2_6/ptodata/2/1na/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	432	2	US-08-313-185-59
2	20	100.0	432	3	US-09-082-614A-59
3	20	100.0	620	2	US-08-757-653-135
4	20	100.0	620	2	US-08-757-653-136
5	20	100.0	620	2	US-08-757-653-137
6	20	100.0	620	2	US-08-757-653-138
7	20	100.0	620	2	US-08-757-653-139
8	20	100.0	620	2	US-08-757-653-140
9	20	100.0	706	4	US-08-797-812-24
10	20	100.0	970	1	US-08-250-030-1
11	20	100.0	970	5	PCr-US95-06790-1
12	19	95.0	19	4	US-08-750-088A-71
13	19	95.0	27	1	US-08-250-030-9
14	15	75.0	27	5	PCr-US95-06790-9
15	14	70.0	3447	2	US-08-313-185-57
16	14	70.0	3447	3	US-09-082-614A-57
17	13	65.0	383	3	US-08-906-769-169
18	13	65.0	383	3	US-08-906-769-169
19	13	65.0	383	3	US-08-639-075A-169
20	13	65.0	383	4	US-09-012-431-169
21	13	65.0	383	4	US-09-012-692-169
22	13	65.0	383	4	US-08-906-613-169
23	13	65.0	537	3	US-08-906-769-171
24	13	65.0	537	3	US-08-906-616-171
25	13	65.0	537	3	US-08-639-075A-171
26	13	65.0	537	4	US-09-012-431-171
27	13	65.0	537	4	US-09-012-692-171

28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, App
30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, App
31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, App
32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, App1
33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, App1
34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, App
35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, App
36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, App
37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, App1
38	12	60.0	391	1	US-08-636-928-6	Sequence 6, App1
39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
40	12	60.0	645	1	US-08-459-586-19	Sequence 19, App
41	12	60.0	645	2	US-08-282-696-19	Sequence 19, App
42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, App1
43	12	60.0	709	1	US-08-459-586-20	Sequence 20, App
44	12	60.0	709	2	US-08-282-696-20	Sequence 20, App
45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/C
Sequence 59, Application US/08313185
Patent No. 581163
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenli, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

THIS PAGE IS BLANK

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGACCC 409

RESULT 2

US-09-082-614A-59/c
Sequence 59, Application US/09082614A
Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenit, Amelio
APPLICANT: Bodmer, Thomas

TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,614A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/313,185

FILING DATE: 12-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356, 0068-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGACCC 409

RESULT 3

US-08-757-653-135/c
Sequence 135, Application US/08757653
Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:

LENGTH: 620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGACCC 277

RESULT 4

US-08-757-653-136/c
Sequence 136, Application US/08757653
Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

This Page Blank (uspto)